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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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Pebruary 7, 2006, 12:49:28 ; Search time 43.8146 Seconds
(without alignments)
9625.515 Million cell updates/sec Run on:

OM nucleic - nucleic search, using sw model

US-10-623-108-5_COPY_1186_1236 51 Perfect score:

1 acagaactggcaaagaggca.....agggcctctgtcacccagga 51 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

19587084 Total number of hits satisfying chosen parameters:

9793542 segs, 4134689005 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:* Published Applications NA_Main:* 8: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	App	App	Appli	Appli	, Ap	, Ap	Appli	Appli	90,	90,	00,	5, A	9, A	, Ap	7, A	8, A	9, A	33,	34,				
u.	668,	668,	7, A	5, A	3351	3351	Э, В	'n	275790	275790	650600	21955,	27809	3069	3070	3069,	3070,	1105		97358	97359	٠,	103734
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
OI	US-09-925-299-668	US-09-925-299-668	US-10-623-108-7	US-10-623-108-5	US-09-764-877-3351	US-10-242-515-3351	US-09-816-095-3	US-10-634-905-3	US-10-027-632-275790	US-10-027-632-275790	US-09-925-065A-650600	US-10-357-930-21955	US-10-357-930-27809	US-09-764-877-3069	US-09-764-877-3070	US-10-242-515-3069	US-10-242-515-3070	US-10-774-355A-1105	US-10-027-632-97357	US-10-027-632-97358	US-10-027-632-97359	US-10-027-632-103733	US-10-027-632-103734
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Query Match	100.0	100.0	100.0	100.0	98.0	98.0	50.2	50.2	48.6	48.6	48.6	48.6	48.6	47.8	47.8	47.8	47.8	47.1	47.1	47.1	47.1	47.1	47.1
Score	51	51	21	51	20	20	25.6	25.6	24.8	24.8	24.8	24.8	24.8	24.4	24.4	24.4	24.4	24	24	24	24	24	24
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C 24	Sequence 103735, A Sequence 97357, A Sequence 97358, A Sequence 97359, A		Sequence 10475, A Sequence 173660, Sequence 2115, Ap Sequence 255989.		Sequence 6668, Ap Sequence 4981, Ap Sequence 6991, Ap Sequence 6778, Ap	Sequence 33612, A Sequence 7, Appli
24 47.1 2112 25 24 47.1 2112 26 24 47.1 2112 28 24 47.1 2112 30 24 47.1 2112 30 24 47.1 2112 31 24 47.1 2112 32 24 47.1 2112 34 23.8 46.7 1562 35 23.8 46.7 1562 36 23.8 46.7 1562 37 23.8 46.7 1562 38 23.8 46.7 1562 39 23.6 46.3 303 40 23.6 46.3 506 41 23.6 46.3 506 42 23.6 46.3 23.8 46.7 24682 39 23.6 46.3 23.8 46.7 24682 39 23.6 46.3 23.8 46.7 24.682 30 23.6 46.3 23.8 46.7 24.682	US-10-027-632-103735 US-10-027-632-97357 US-10-027-632-97358 US-10-027-632-97359	US-10-027-632-103733 US-10-027-632-103734 US-10-027-632-103735 US-10-057-475B-10475	US-10-154-884B-10475 US-10-425-115-173660 US-10-106-698-2115	US-10-027-632-255989 US-10-103-313-132 US-10-235-192A-28 US-10-006-285-5	US-10-029-386-6668 US-10-723-860-4981 US-10-719-993-6991 US-10-719-993-6778	US-10-425-115-33612 US-10-225-810-7
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## ALIGNMENTS

RESULT

US-09-92\$-299-668

ORGANISM: Homo sapiens NAME/KEY: misc feature TYPE: DNA FEATURE:

υ υ υ υ O ò ö ö ö ö LOCATION: (8)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (1727
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (2397 OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc_feature LOCATION: (243) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (329) LOCATION: (243)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature

O O U or or ö LOCATION: (353) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc_feature a,t,g, INFORMATION: n equals a,t,g, OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (353) NAME/KEY: misc feature LOCATION: (330) LOCATION OTHER

LOCATION:

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RESULT/ 5
US-09-764-877-3351
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sequence 660 No. US20030040617A9
publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT FILING DATE: 2001-08-10
PRIOR PELICATION NUMBER: DCT/US00/05883
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 668
LENGTH: 365
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                                                                                                                                  Query Match 100.0%; Score 51; DB 3; Length 365; Best Local Similarity 100.0%; Pred. No. 2.8e-10; Matches 51; Conservative 0; Mismatches 0; Indels
                OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (362)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-668
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NOMER INFORMATION: n equale a,t,g, or c
NAME/KEY: misc feature
LOCATION: (362)
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US-09-925-299-668
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LOCATION: (353)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (358)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
TOCATION: (330)
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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US-09-925-299-668
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18-10-623-108-7
| Sequence 7, Application US/10623108
| Publication No. U22050013817A1
| Sequence 7, Application No. U22050013817A1
| Publication No. U22050013817A1
| APPLICANT: DAI, KEN-SHWO
| TITLE OF INVENTION: HUMAN SWAPK3-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS
| FILE REPERENCE: U 014726-8
| CURRENT APPLICATION NUMBER: US/10/623,108
| CURRENT FILING DATE: 2003-07-18
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 7
| LENGTH: 1777
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Patent No. 1952020147140a1

Patent No. 19520020147140a1

Patent No. 19520020147140a1

GENERAL INFORMATION:

APPLICANT: ROSE et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PCOO5

CURRENT PAPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3351
  1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA
                              32 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA
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Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 51; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DAI, KEN-SHWO
TITLE OF INVENTION: HUMAN SWAPK3-RELATED
FILE REFERENCE: U 014726-8
CURRENT APPLICATION NUMBER: US/10/623,108
CURRENT FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-623-108-5
; Sequence 5, Application US/10623108
; Publication No. US20050013817A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-623-108-7
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ORGANISM: Homo sapiens
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RESULT 9
US-10-027-632-275790
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US-10-634-905-3
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TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOL147
CURRENT APPLICATION NUMBER: US/09/816,095
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6375 ACAGAACTGGCAAAGAGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG 6424
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOSCI
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR PILING DATE: 2000-01-7
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
                                                                                                                                ch 98.0%; Score 50; DB 3; Length 13808; Similarity 100.0%; Pred. No. 9.6e-10; 50; Conservative 0; Mismatches 0; Indels
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Pred. No. 9.6e-10;
                                                                                                                                                                                                                                                             1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG
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100.0%; Pred. No. ...
0; Mismatches
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Patent No. US20020137164A1
GENERAL INFORMATION:
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US-10-242-515-3351
                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3351
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                            Query Match
Best Local Similarity
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LENGTH: 13808
LENGTH: 13808
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                                                                                                                                                                                                      Matches
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Sequence 3, Application US/10634905
Publication No. US20040067225A1
GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: THEREOF
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; Sequence 275790, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
; TITLE OF INVENTION: Polymorphisms in the Human Genome
    TITLE OF INVENTION: POLYMORER: US/10/027,632
    CURRENT FILING DATE: 2000-04-30
    PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/185,218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
50.2%; Score 25.6; DE
Best Local Similarity 70.8%; Pred. No. 6.2;
Matches 34; Conservative 0; Mismatches
CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 99916

TYPE: DNA

PRATURE:
NAME/KEY: misc_feature

LOCATION: (1)...(99916)

CUCHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(99916)

CTHER INFORMATION: n = A,T,C or G

US-10-634-905-3
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ORGANISM: Homo sapiens
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APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE
TITLE OF INVENTION: HUMAN: 09/185, 276
FRICK FILING DATE: 2003-02-04
FRICK FILING DATE: 2000-02-17
FRICK FILING DATE: 2000-02-17
FRICK FILING DATE: 2000-03-16
FRICK FILING DATE: 2000-06-25
FRICK FILING DATE: 2000-06-25
FRICK FILING DATE: 2000-06-25
FRICK FILING DATE: 2000-06-18
FRICK FILING DATE: 2000-06-09
FRICK FILING DATE: 2000-06-18
FRICK FILING DATE: 2000-06-18
FRICK FILING DATE: 2000-06-18
FRICK FILING DATE: 2000-07-18
FRICK FILING DATE: 20
     TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Pred. No. 8.5;
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                                                                                                            CURKENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-16
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                                                         FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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US-10-357-930-21955
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Matches 32, Conservative
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US-09-925-065A-650600
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Best Local Similarity
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; Sequence 275790, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/198,676
; PRIOR PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR PELING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR PELING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/15,363
; PRIOR PILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-00-02-24
; PRIOR FILING DATE: 1999-00-02-3
; PRIOR PILING DATE: 1999-09-08-09
; PRIOR PILING DATE: 1999-09-08-09
; PRIOR PILING DATE: 1999-09-08-09
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; Sequence 650600, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TGGCAAAGAGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA
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; Pred. No. 8;
0; Mismatches
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-9
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FREUSER FOR WINDOWS VERSION 4.0
SOFTWARE: PREUSER FOR WINDOWS VERSION 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 275790
LENGTH: 506
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Best Local Similarity 72.7%;
Matches 32; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-027-632-275790
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ORGANISM: Human
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Search completed: February 7, 2006, 15:20:14
Job time : 44.8146 secs
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US-09-764-877-3070
US-09-764-877-3069
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Sequence 27809, Application US/10357930

Sequence 27809, Application US/10357930

Sequence 27809, Application No. US20040259086A1

GENERAL INFORMATION:
APPLICANT: Endege. Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: IDENTIFICATION WABER: US/10/357,930
CURRENT APPLICATION NUMBER: 09/785,276
FRIOR FILING DATE: 2003-02-04
FRIOR FILING DATE: 2003-02-16
FRIOR FILING DATE: 2000-03-16
FRIOR FILING DATE: 2000-03-16
FRIOR PILING DATE: 2000-03-16
FRIOR FILING DATE: 2000-03-16
FRIOR FILING DATE: 2000-03-16
FRIOR FILING DATE: 2000-05-25
FRIOR FILING DATE: 2000-06-25
FRIOR FILING DATE: 2000-06-07-18
FRIOR FILING DATE: 2000-07-18
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Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT APPLICATION UNMERR: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper;

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 3069

LENGTH: 331
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Pred. No. 8.5;
0; Mismatches 12; Indels
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                                                                        1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCA 44
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US-10-357-930-27809
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Best Local Similarity 72.7%;
Matches 32; Conservative
       32; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 3700, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: WOLCHIC Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT PFLING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3070

LINGTH: 331
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47.8%; Score 24.4; DB 3; Length 331; 73.8%; Pred. No. 11; Live 0; Mismatches 11; Indels
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Best Local Similarity 73.84
Matches 31; Conservative
    Query Match
Best Local Similarity 73.84
Matches 31; Conservative
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US-09-764-877-3070
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Scoring table:

Searched:

Database

Perfect score:

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Sequence:

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/clone lib="NH MGC 19"
/clone lib="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2:
RooRi, cDNA made by oligo-dr priming. DIrectionally
cloned into BcoR/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
AL153256 Anopheles
CK607655 Controlb
CV999827 iv53407.9
CA758516 OP13801-T
DN10644 1103825 M
BR437662 B8437662
BL182540 UNL-P-N-
CJ030128 CJ030128
CB29831 220018 re
AQ877413 HS 2146_A
A1450334 MUZ7609.x
AL045331 DKFZp434A
BL175907 BST51690
BM175907 BST51690
                                                                                                                                                                                                                                  AW888774 RCO-NTO1
BP569448 RCO-GNO9
BG552612 df44g10.x
AL488207 T. brucei
CE337026 tigr-g88-
BU4533301 603808454
BU453132 603218139
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1. (bases 1 to 555)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
Plate: LLCM313 row: a column: 19
High quality sequence stop: 505.

Location/Qualifiers
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BG552612
TA269G09Q
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BI175907
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AI450334
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BU456559
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Homo sapiens
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AUTHORS
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BM041252 60361446
CA446812 UT-H-ED1-
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BS50582 CIT-HSP-494
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BF675069 60213667
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CV358408 PMO-AN008
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BI869166 603395496
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AQ207132 HS 3235 A
CV320055 CMS-UT0<sup>0</sup>8
AQ428895 CITBI-E1-
CN244360 EST010237
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                                                                                                                February 7, 2006, 12:29:45; Search time 200.677 Seconds (without alignments) 11890.431 Million cell updates/sec
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                                                                                                                                                                                                             1 acagaactggcaaagaggca.....aggggcctctgtcacccagga 51
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                                                                                                                                                                                                                                                                                                                         82156650
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                          41078325 seqs, 23393541228 residues
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51
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM nucleic - nucleic search, using sw model
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AA324242
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Maximum DB seq length: 200000000
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Match Length DB
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9b_est6:*
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9b_est7:*
9b_gs82:*
9b_gs83:*
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37.4 37.4 228.4 27.8

Score

Result

51 51 51 51 51 51

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26.6 26.4 26 26 26

8 110 111 111 113 114 117 118 119 119 119 119

25.8 25.8 25.8 25.8

Gaps

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21

Matches

EST

KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL PUBMED

COMMENT

DEFINITION

RESULT 2 BM702058

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ACCESSION VERSION

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BE891264 653 bp mRNA linear EST 20-OCT-2000 601432092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917255 5',
                                                                                                                                                                                                                                                                    CB156158 575 bp mRNA linear EST 29-JAN-2003
K-EST0214813 L18POOLIN1 Homo sapiens CDNA clone L18POOLIN1-2-C09
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="LighOoLin1"
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laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                         1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCCAGGA 51
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100.0%; Pred. No. 3.7e-07;
ive 0; Mismatches 0;
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0; Mismatches
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BE891264.1 GI:10350423
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Homo sapiens
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/ Ob Xref="mRNA#"
/ (db Xref="mRNA#"
/ (db Xref="mRNA#"
/ (clone="ul-E-CQ1-aey-e-05-0-UI"
/ (issue type="adult"
/ (dev stage="adult"
/ (dev stage="adult"
/ (dev stage="adult"
/ (dome lib="ulr-B-CQ1"
/ (dome lib="adult"
/ (dome Research, 6:791-806, 1996. First strand cDNA
/ (dome Research, 6:791-806, 1996. First strand c
                                                                                                                                                                                                                                                                                                                                 ым/идо58
UI-B-CQ1-aey-e-05-0-UI.rl UI-B-CQ1 Homo sapiens cDNA clone
UI-B-CQ1-aey-e-05-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Dento-goares@ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 555)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                               Gaps
                                                                                                                                                                                         309 ACAGAACTGGCAAAGAGGGCAAGAGGGGTCACTGAGGGCCTCTGTCACCCAGGA 359
                                                                                                                                                       51
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9250
Fax: 319 335 9565
                                                                                                                                                       1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA
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                              100.0%; Score 51; DB 2; Length 555; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NNH MGC 72"
/note="Organ: Skin; Pector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM041252 673 bp mRNA linear EST 07-NOV-200
603614446F1 NIH_MGC_108 Homo sapiens cDNA clone IMAGE:5420314 5',
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCA1874 row: 1 column: 11
High quality sequence stop: 648.
                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9743 row: h column: 24
High quality sequence stop: 602.
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1 (bases 1 to 673)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 653)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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100.0%; Pred. No. 3.7e-07;
tive 0; Mismatches 0;
                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3917255"
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/db_xref="taxon:9606"
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/clone="IMAGE:5420314"
/tissue_type="Wilms' tumor, cell line"
/lab_host="WhlDB (phage-resistant)"
/clone_lib="WilH MGC_108"
/clone_lib="WilH MGC_108"
/clone_Torgan: kidney; Vector: pOTB7; Site_l: Xhol; Site_2:
ECORI, cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/Xhol sites using the following 5; adaptor:
GGACGAG(1. Library constructed by Ling Hong in the
laboratory of Garald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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// Ab_xref="taxon:9606"
// Ab_xref="taxon:9606"
// Aboxe="mrkNa"
// Lissue_type="Chondrosarcoma"
// Lissue_type="Chondrosarcoma"
// Lissue_type="Chondrosarcoma"
// Aboxe="Malt"
// Aboxe="Malt"
// Aboxe="Malto"
// Aboxe="Malto
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Contract: Robert Miniburgov
Tissue Procurement: Dr. Jose Mercuende
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seg primer: M13 FORWARD
POUYA=Yes.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 673)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Score 51; DB 3; I
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 51; Conservative 0; Mismatches 0;
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Infullibrary now, the set, in the set of the set of the set of set of the sequence version replaced gi:31314903.

Li,W.B., Gruber.C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:31314903.

Contact: Genoscope

Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@egnoscope.cns.fr, Web : www.genoscope.cns.fr

Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pchysporT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B50582 linear GSS 20-JUN-1998 CIT-HSP-494012.TV CIT-HSP HOMO Sapiens genomic clone 494012,
                                                      EST 07-APR-2004
                                                         AL576621 AL576621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI078YM11 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CSODIO78YM1".
/clone="TAPE="PLACENTA COT 25-NORWALIZED"
/clone lib="Home sapiens PLACENTA COT 25-NORWALIZED"
/note="lib strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-extrand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Determination of clone end sequences of human Bacterial Artificial
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI078AG06NP1&c=8342.f. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:9606"
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Unpublished (1997)
Contact: Ung-Jin Kim
CalTech Genome Research Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
                                                                                                                                   AL576621
AL576621.3 GI:46255607
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          RESULT 8
AL576621/c
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AUTHORS
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/dlone="IMAGE:5420314"
/tlseue_type="wilms' tumor, cell line"
/lab host="bH10B (phage-resistant)"
/clone_lib="NIH MGC_108"
/clone_lib="NIH MGC_108"
/clone="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site_2:
RcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT. TAG_TISSUE-chondrosarcoma TAG_ILB=UI-H_ED1 TAG_SEQ=CGTCAAGGCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM041386 773 bp mRNA linear EST 07-NOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov.
Plate: LLCM1874 row: 1 column: 11
High quality sequence start: 26
High quality sequence stop: 718.
Location/Qualifiers
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1 (bases 1 to 773)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                            611 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 561
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                                                                                                                                                                                        ch 100.0%; Score 51; DB 6; Length 673; 1 Similarity 100.0%; Pred. No. 3.7e-07; 51; Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM041386.1 GI:16770653
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Gaps

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unamplified): hd/he"
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BF675069
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1 (bases 1 to 520)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Wistow,G., Bernstein,S.L., Wyatt,M.D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
Mol. vis. 8 (4), 196-204 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BO640705 520 bp mRNA linear BST 15-JUL-2002 hellboo.yl Human Retina cDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone hellboo?', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
California Institute of Technology
Division of Biology, MS 147-75, Pagadena, CA 91125, USA
Division of Biology, MS 147-75, Pagadena, CA 91125, USA
Division of Biology, MS 147-75, Pagadena, CA 91125, USA
Fax: 626 395 4901
Email: ung@ash.tree.caltech.edu
Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: graeme@helix.nih.gov
Plate: 32 row: b column: 09
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.8%; Score 46.8; DB 9 96.0%; Pred. No. 1e-05; ive 0; Mismatches
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                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="GDB:5420786"
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/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                          db_xref="taxon:9606"
clone="494012"
                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative
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Fax: 301 496 0078
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                                                                                                                                                                                                                         1. .307
                                                                                                                                                                       Seg primer: T7
Class: BAC ends.
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Best Local Similarity
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셤 δ

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/.d. Atter-_cardunisty.
/.d. Atter-_cardunisty.
/lab_host="DH10B (T1 phage-resistant)"
//clone lib="NIH MGC 83"
//clone lib="NIH MGC 83"
//note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: Sfil (ggocgoctegggc); Site 2: Sfil
(ggocattatggc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCATATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCATATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCATATGGCC-3'
C, or G and N = A, C, G, or T). Average insert size 1.4
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
Integration in the control of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer-adapter

[A. pda.ThdfTTCTAGATCGCGAGCGGCCG(T) 15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.

The sub-procurement: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1088 row: e column: 18

High quality sequence stop: 649.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominida, Latarinini, Latarinini, Latarinini, Latarinini, 1 (base; Homo.)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.4; DB 5; Length 520;
Pred. No. 0.023;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAGGCAAGAGGCACTGAGGCCTCTGTCACCAGGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF675069.1 GI:11948964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.4%;
Matches 38; Conservative 0
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DEFINITION

RESULT 12 AA324242

Matches

ORIGIN

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_tref="acxon:9606"
/db_tref="acxon:9606"
/dev_stage="Adult"
/clone_lib="AN0087"
/note="forgan: amnion_normal; Vector: pucl8; Site_1: Smal;
/note="forgan: amnion_library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Ociles into one Ociles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae, Homo.

1 (bases 1 to 412)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE385462 680 bp mRNA linear EST 21-JUL-2000
601276049F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616813 5',
                                                                                                                                                                                     CV358408 412 bp mRNA linear EST 27-SEP-2004
PMO-AN0087-270101-008-g09 AN0087 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.5%; Score 27.8; DB 7; Length 412; Best Local Similarity 74.5%; Pred. No. 53; Matches 35; Conservative 0; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG
                                                   405
47
8 TGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCC
                               366 TGGCAAAGGGCAAGAGGTCATTGAGGGGCNTTTTNACC
                                                                                                                                                                                                                                                                        CV358408.1 GI:52708463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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ORGANISM
                                                                                                                                                                                                                    DEFINITION
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COMMENT
                                                                                                                                    RESULT 13
CV358408
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VERSION
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BE385462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                        KEYWORDS
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  8
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Hominidae; Homo.

1 (Dasea; 1 to 500)

Rdams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstnetock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,

Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblow,E., Hinkle,P.S.Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Bednarik,D.P., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Liw,W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,

Raymond,L., Weil,Y.F., Wing,J., Xu,C., Yu,G.L., Haseltine,W.A., Flelds,C.,

Praser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                            AA324242 500 bp mRNA linear EST 20-APR-1997 EST27116 Cerebellum II Homo sapiens CDNA 5' end similar to EST containing Alu repeat, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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/clone_lib="Cerebellum II"
//note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
                                                                                   Gaps
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                                                                                                                                                                      0;
                                                                                                                                       1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 51
                                                                                   ;
                            73.3%; Score 37.4; DB 2; Length 855; 96.1%; Pred. No. 0.024;
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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/db_xref="ATCC (inhost):124792"
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                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.7%;
Best Local Similarity 80.0%;
Matches 32; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                      49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                         Best Local Similarity
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                                  Query Match
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JOURNAL PUBMED

COMMENT

TITLE

FEATURES

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Gaps

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92

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Search completed: February 7, 2006, 14:53:04 Job time : 204.677 secs
High quality sequence stop: 539.
Location/Qualifiers
                     FEATURES
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tisaue Procurement: ATCC/bCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Parayed by: The I.M.A.G.E. Consortium (ILINL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiML at: image.llnl.gov
Plate: LLCM283 row: b column: 14
High quality sequence stop: 617.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12033 row: p column: 23
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1 (bases 1 to 698)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                Hominidae; Homo.
1 (bases 1 to 680)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 ACAGAGGTCTCAAAGACCCCAGAGGACTCGGGAGGCACCTGCCACCGGGA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.9%; Score 27; DB 2; 70.6%; Pred. No. 1.1e+02; tive 0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:3616813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI869166.1 GI:16042826
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Best Local Similarity
Matches 36; Conservé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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JOURNAL
COMMENT
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AUTHORS
                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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/notes="Organ: Ilver; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650 AGAAGGGTAAATAGTGAAGGGGGAGCTGAGGCCTTGAGTCACCCAGGA 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.2%; Score 26.6; DB 3; Length 698; Best Local Similarity 71.4%; Pred. No. 1.5e+02; Matches 35; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA
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/clone="IMAGE:5405446"
/tissue_type=adenocarcinoma, cell line"
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/clone_lib="NIH_MGC_90"
1. .698
/organism="Homo sapiens"
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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OM nucleic - nucleic search, using sw model

7, 2006, 12:22:44; Search time 31.0376 Seconds (without alignments) 10951.209 Million cell updates/sec February Run on:

US-10-623-108-5_COPY_1186_1236 51 score:

1 acagaactggcaaagaggca.....agggcctctgtcacccagga 51 Sequence: Perfect

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4996997 segs, 3332346308 residues Searched:

9993994

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs: geneseqn2003as:* geneseqn2003bs:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* N_Geneseq_21:* 10: •• Databaве

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn20058:*

## SUMMARIES

	Description		Aac98658 Human col	Acn41203 Human dia	Acn41200 Human dia	Acn41199 Human dia	Adw12906 Human SMA	Adw12904 Human SMA	. Aal36986 Human mus	Abx59974 cDNA enco	Adj30724 Human mus	Adi03931 Human enz	Adq97587 Human can	Abv21964 Human pro	Abv27796 Human pro	Aal36705 Human mus	Aal36704 Human mus	Abx59692 cDNA enco	Abx59693 cDNA enco	Adj30443 Human mus	Adj30442 Human mus
	ID		AAC98658	ACN41203	ACN41200	ACN41199	ADW12906	ADW12904	AAL36986	ABX59974	ADJ30724	ADI03931	ADQ97587	ABV21964	ABV27796	AAL36705	AAL36704	ABX59692	ABX59693	ADJ30443	ADJ30442
	DB	-	٣	13	13	13	14	14	4	œ	12	ø	12	Ŋ	Ŋ	4	4	œ	œ	12	12
	Query Match Length DB		365	1210	1290	1305	1777	1837	13808	13808	13808	99916	116297	992	992	331	331	331	331	331	331
æ	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	98.0	98.0	98.0	50.2	50.2	48.6	48.6	47.8	47.8	47.8	47.8	47.8	47.8
	Score		51	51	51	51	51	51	50	20	20	25.6	25.6	24.8	24.8	24.4	24.4	24.4	24.4	24.4	24.4
	Result No.		ч	7	6	4	S	v	7	60	σ	10	11	12	13	14	15	16	17	18	19

Acl73128 M. xanthu	Ac164626 M. xanthu	Aac74422 Human sec	Abz73645 Secreted	Ada98137 Human sec	Abz67239 Human sec	Aac93331 Human sec	Aah35023 Human col	Adu82622 Human MDD	Aas34888 cDNA enco	Adc46046 Human neo	Adl08109 Human gen	Adi22195 Rat liver	Ach73473 Human gen	Adq22161 Human sof	Ada41546 Human sec	Ada57677 BAC fragm	Abz80234 Mouse tra	Adm01710 Human cDN	Adb62760 Human cDN	Adr08430 Full leng	Aba20479 Human ner	Add47140 Human gen	Add14677 Human Brc	Adr52965 Drug ther	Aai18474 Probe #84	
ACL73128	ACL64626	AAC74422	ABZ73645	ADA98137	ABZ67239	AAC93331	AAH35023	ADU82622	AAS34888	ADC46046	ADL08109	ADI22195	ACH73473	ADQ22161	ADA41546	ADA57677	ABZ80234	ADM01710	ADB62760	ADR08430	. ABA20479	ADD47140	ADD14677	ADR52965	AAI18474	
14	14	m	∞	ω	10	m	4	13	4	10	12	ដ	12	12	æ	20	œ	11	10	13	ß	2	10	13	4	
.1023	13346	1008	1008	1008	1008	1043	1312	2140	3863	3863	247682	303	206	7862	2932	2932	17173	1756	3089	3356	11706	28564	34875	34875	226	
47.8	47.8	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.3	46.3	46.3	45.9	45.9	45.9	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.1	
24.4	24.4	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.6	23.6	23.6	23.4	23.4	23.4	23.2	23.2	23.2	23.2	23.2	23.2	23.2	23	
20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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## ALIGNMENTS

AAC98658 standard; cDNA; 365 BP. AAC9865,

RESULT

AAC98658;

(first entry) 09-MAR-2001 Human colon cancer antigen nucleotide sequence SEQ ID NO:668.

identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss. Human; colon cancer; colon cancer antigen; diagnosis; detection;

WO200055351-A1.

Homo sapiens

21-SEP-2000.

08-MAR-2000; 2000WO-US005883.

99US-0124270P. 12-MAR-1999; (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2000-587534/55. P-PSDB; AAB53901.

Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.

Claim 1; Page 1200; 2104pp; English.

AAC97991 to AAC98763 encode the human colon cancer associated proteins,

```
called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardiactive, muscular; neuroprotective, immunomodulatory, gymaecological, gastrointestinal, vulnerary, nephrotropic, antilinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, correlated and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC9874 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 51 32 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 82 Human diagnostic and therapeutic polynucleotide SEQ ID NO:78. ACN41203 standard; cDNA; 1210 BP (first entry) 18-NOV-2004 ACN41203; RESULT 2 ACN41203 셤 ò

 $ss\,;$  gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

12-SEP-2003; 2003WO-US028227. 2002US-0410259P. WO2004023973-A2. Homo sapiens. 12-SEP-2002; 12-SEP-2002; 25-MAR-2004. 

(INCY-) INCYTE CORP

Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Markhshorne TA, Suchorolski MT, Altus CM, Pittes SJ, Balder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Paneer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Policky JL, Suarez CJ; Rb, Kwong M, Shi X, Patury S,

WPI; 2004-329368/30. P-PSDB; ABM82551

New diagnostic and therapeutic polynuclectides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 1; Page; 190pp; English

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A

Claim 1; Page; 190pp; English.

in gene mapping.

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diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine disorder. Intlammatory disorder, developmental disorder, endocrine disorder, enuclogical disorder, developmental disorder, endocrine disorder, enuclogical disorder, parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Blder LV;
Hooney ZM, Delegeare AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 1024 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCCAGGA 1074
                                                                                                                                                                                                                                                          directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                           51
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human diagnostic and therapeutic polynucleotide SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                             1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCCTCTGTCACCCCAGGA
                                                                                                                                                                                                                                                                                            Sequence 1210 BP; 248 A; 375 C; 376 G; 211 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 13;
100.0%; Pred. No. 3.8e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN41200 standard; cDNA; 1290 BP
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12-SEP-2002; 2002US-0410260P.
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABM82548.
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polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autolomnune/inflammatory disorder, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conjumented biological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conjumented may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

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Gaps

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Indels

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; Score 51; DB 13; ; Pred. No. 3.8e-09; 0; Mismatches 0;

ch 100.0%; 1 Similarity 100.0%; 51; Conservative 0

Query Match Best Local 8

Best Loc Matches

8

Length 1305;

Sequence 1305 BP; 273 A; 411 C; 392 G; 229 T; 0 U; 0 Other;

1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 51

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ö
polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, associated autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or gérmline gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 13; 100.0%; Pred. No. 3.8e-09;
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ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
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                                                                                                                                                                                                                                                                                 Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthbhorne TA, Suchorolski MT, Altus CM, Pitts SJ, Edder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioure P, Shen EJ, Wu MC, Stuve LL; Liagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer
                                                                           Human diagnostic and therapeutic polynucleotide SEQ ID NO:74.
          ACN41199 standard; cDNA; 1305 BP
                                                                                                                                                                                                                           12-SEP-2002; 2002US-0410259P.
                                                                                                                                                                                                     12-SEP-2003; 2003WO-US028227
                                                       (first entry)
                                                                                                                                                                                                                                                            (INCY-) INCYTE CORP.
                                                                                                                                                         WO2004023973-A2
                                                                                                                                     Homo sapiens
                                                      18-NOV-2004
                                                                                                                                                                                25-MAR-2004.
                                 ACN41199
                                                                                                              ditho.
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A

Claim 1; Page; 190pp; English.

gene mapping

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

Suarez CJ;

Shi X,

Patury S,

WPI; 2004-329368/30.

P-PSDB; ABM82547.

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New isolated SWAPK3 polypeptides and nucleic acids, useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SWAPK3 gene in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel isolated polypeptide (I) comprising an amino acid sequence selected from sequences comprising 335 or 359 amino acids (ADW12901 or ADW12903) or its fragments. The polypeptides and polymucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SWAPK3 gene in a mammal. The fragments of the polypeptides and polymucleotides can also be used as
                                                                                                                                                                                          DNA purification; diagnosis; cancer; mitogen-activated protein kinase;
1119 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCCAGGA 1169
                                                                                                                                                                                                                                                                                                      /product= "SMAPK3V4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 7; 55pp; English.
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                  ADW12906 standard; cDNA; 1777
                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2003; 2003US-00623108.
                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2003; 2003US-00623108
                                                                                                                                                                  Human SMAPK3V4 variant gene.
                                                                                                                                                                                                                                                                          12. .1091
/*tag= a
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-080923/09.
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                                                                                                                                                                                                                                                                                                                                   US2005013817-A1.
                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                        07-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                            (DAIK/) DAI
                                                                                                                                                                                                                                                                                                                                                            20-JAN-2005
                                                                                                             ADW12906;
                                                                                                                                                                                                            gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dai K;
                                                       RESULT 5
ADW12906
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AAL36986 standard; DNA; 13808 BP.
                                                                         (first entry)
                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                     16-MAR-2000;
17-MAR-2000;
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02-MAR-2000;
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                                                                         08-JAN-2002
                                                                                                                                                                                                               02-AUG-2001
                                                        AAL36986;
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                    RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated SMAPK3 polypeptides and nucleic acids, useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino
                                                                                                                                                                                                                        purification; diagnosis; cancer; mitogen-activated protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel isolated polypeptide (I) comprising an amino acid sequence selected from sequences comprising 335 or 359 amin acids (ADW12901 or ADW12903) or its fragments. The polypeptides and polynucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SWAPK3 gene in a mammal. The fragments of the polypeptides and polynucleotides can also be used as primers or probes. This sequence corresponds to the CDNA encoding the
primers or probes. This sequence corresponds to the cDNA encoding the SMAPK3V1 variant protein.
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                                                                  Gaps
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                                                Length 1777;
                                                                                   1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCCAGGA
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                               Sequence 1777 BP; 355 A; 575 C; 507 G; 340 T; 0 U; 0 Other;
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                                                                  Indels
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100.0%; Pred. No. 4.1e-09;
ive 0; Mismatches 0;
                                                Score 51; DB 14;
Pred. No. 4.1e-09;
                                                                                                                                                                                                                                                                                               /product= "SMAPK3V3 protein"
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 5; 55pp; English.
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                  ADW12904 standard; cDNA; 1837 BP
                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2003; 2003US-00623108
                                                                                                                                                                                                        Human SMAPK3V3 variant gene
                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                             . .1151
                                                                  51; Conservative
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les 51; Conserv
                                                         Best Local Similarity
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                                                                                                                                                                                      07-APR-2005
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                                                                                                                                                                    ADW12904;
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Matches
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1186 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGGA 1236

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
Human musculoskeletal system related polynucleotide SEQ ID NO 3351.
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2000US-0225757P.
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                                                                                                                                                                                                       musculoskeletal system; ds
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08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0232080P.
14-SEP-2000; 2000US-0232081P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-0232306P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-0233065P.
21-SEP-2000; 2000US-0233065P.
21-SEP-2000; 2000US-0233065P.
21-SEP-2000; 2000US-0233063P.
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2000US-0234274P.
2000US-0234998P.
2000US-0235484P.
2000US-0235484P.
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2000US-0236802P.
2000US-0237037P.
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2000US-0240960P.
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2000US-0241808P.
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25-SRP-2000; 2
27-SRP-2000; 2
27-SRP-2000; 2
27-SRP-2000; 2
29-SRP-2000; 2
29-SRP-2000; 2
29-SRP-2000; 2
29-SRP-2000; 2
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17-NOV-2000; 2
17-NOV-2000; 2
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01-NOV-2000;
08-NOV-2000;
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The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein cor gene therapy. The genes are isolated from a range of human tissues circ giacalosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, clung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, calbetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arbititis and ulcerative colitis; (c) cardiovascular disorders such as cerebral anoxia and epplepsy; and (f) infections diseases such as viral, cerebral anoxia and epplepsy; and (f) infections diseases such as viral, correctal, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was correctant the patent did not format directly from WIPO at corpus for the printed for the printed specification, but was corpus for the printed in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13808 BP; 2990 A; 3953 C; 3656 G; 3209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding novel human musculoskeletal system antigen #2318.
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                               17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250191P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-025199P.
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nes 50; Conservative
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post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; Parkinson's disease; Parkinson's disease; Parkinson's disease; Parkinson's disease; parbarication; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; nair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight, hair colour; skin; percentage of adipose tissue; pigmentation; commetic surgery; metabolism; blorhythm; caricadic rhythm; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content; 11-JUL-2000; 2000US-0217487P. 2000US-0226868P 2000US-0229343P 2000US-0229509P 2000US-0229513P 2000US-0234223P 2000US-0234274P 2000US-0235834P 2000US-0236368P 2000US-0236369P 2000US-0237039P 2000US-0237040P 17-JAN-2001; 2001US-00764877 07-JUL-2000; 2000US-0216647P 07-JUL-2000; 2000US-0216880P 2000US-0237038P 2000US-0241809P 2000US-0251869P nutritional component US2002147140-A1 02-OCT-2000; 13-OCT-2000; 20-OCT-2000; Homo sapiens. 08-SEP-2000; 29-SEP-2000; 02-OCT-2000; 08-DEC-2000; 20-OCT-2000; 05-SEP-2000; 10-OCT-2002 14-AUG-2000 14-AUG-2000 L4-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 22-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 27-SEP-2000 -SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 -OCT-2000 -OCT-2000 14-AUG-2000 

The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful conference or cancer metaseases, in animals or for detecting disorders, e.g., cancer or cancer metaseases, in animals or thumans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; preats wounds due to injuries, and other candiovascular conditions; preats wounds due to injuries, and limb regeneration; stimulates neuronal growth; can treat and prevent conditions, such as, Albriemer's disease, Parkinson's disease, and AlDS-conditions, stimulates chondrocyte growth, thus they can be used to retract a periodontal regeneration and aid in tissue transports or retrained in combination of home promotes melanocyte growth; grewents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates of growth and differentiation of hometopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryonic seem cells, besides, haematopoietic lineage; modulates mammalism colour, este colour, seem cells, besides, haematopoietic lineage; modulates mammalism colour, see commett surgery); modulates mammalism metabolism; changes mammalism estate by highsel state or physical state by highsel state or physical state by highsel state or physical state or physical state by highsel state or physical st ö musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis; gene therapy; vaccine; human; ds. Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer. Gaps Human musculoskeletal system-associated genomic DNA - SEQ ID 3351. Sequence 13808 BP; 2990 A; 3953 C; 3656 G; 3209 T; 0 U; 0 Other; 6375 ACAGNACTGGCAAAGAGGCAAGAGTCACTGAGGGCCTCTGTCACCCAGG 6424 ö 1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG 50 98.0%; Score 50; DB 8; Length 13808; 100.0%; Pred. No. 1.5e-08; 0; Indels ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140 100.0%; Prea. ww. Disclosure; SEQ ID NO 3351; 321pp; English ADJ30724 standard; DNA; 13808 BP. Barash SC; 20-MAY-2004 (first entry) 50; Conservative Ruben SM, WPI; 2003-128199/12 Best Local Similarity (RUBE/) RUBEN S M. (BARA/) BARASH S C. Rosen CA, ADJ30724; Query Match Matches ADJ30724 8XXXXXXXXXXXX ò

Homo sapiens

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2000US-0235834P.
2000US-023634P.
2000US-023634P.
2000US-023636P.
2000US-0236370P.
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   2000US-0179065P

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2000US-022964P

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                    US2004009488-A1
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26-JUL-2000;

14-AUG-2000;

18-AUG-2000;

18-AUG-2000;

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19-AUG-2000;

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                                                                                                  The invention relates to a novel isolated musculoskeletal system-
sesociated nucleic acid molecule. The nucleic acid of the invention
demonstrates cytostatic and osteopathic activities and may be useful for
preparing a medicament for preventing, treating or ameliorating a medical
condition such as cancer of the musculoskeletal tissues or osteoporoals,
possibly via en therapy or vaccine production. The current sequence is
that of the human musculoskeletal system-associated genomic DNA of the
                                                                                                                                                                invention. The current sequence is not shown within the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20040009488.
                                            New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer of musculoskeletal tissues or osteoporosis.
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                                                                                                                                                                                                      Sequence 13808 BP; 2990 A; 3953 C; 3656 G; 3209 T; 0 U; 0 Other;
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                                                                                                                                                                                                                          Length 13808;
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Local Similarity 100.0%; Pred. No. 1.5e-08;
ies 50; Conservative 0; Mismatches 0;
                                                                                  Disclosure; SEQ ID NO 3351; 289pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Human enzyme protein encoding genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "enzyme protein"
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         Barash SC;
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/number= 3
96832. .96915
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64458. .96602
/*tag= e
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96752. .96831
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/*tag= f
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                            WPI; 2004-090458/09
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          Rosen CA,
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preferentially expressed. The human enzyme protein is also userul for diagnosing a disease, predisposition to a disease, or treating a disorder characterized by an absence of, inappropriate or unwanted expression of the protein. The antibodies are useful in pharmacogenomic analysis, for inhibiting protein function, or for tissue typing. The nucleic acid molecules are useful as probes, primers, othemical intermediates, or in molecules are useful as probes, primers, othemical intermediates, or in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated enzyme protein and encoding polymucleotides. The protein shows a high degree of similarity to a glucuronyltransferase cloned from a rabbit brain cDNA library. The peptides and mucleic acid melecules are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents. The peptide may be used in drug screening assays, in assays to determine the biological activity of the protein, to raise antibodies or to elicit another immune response, as a reagent in assays elessigned to quantitatively determine levels of the protein in biological fluids, or as markers for tissues in which the corresponding protein is preferentially expressed. The human enzyme protein is also useful for as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human enzyme proteins, useful for treating or diagnosing disorders associated with abnormal expression of the protein, in drug screening
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Pred. No. 40;
0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Di Francesco V, Beasley EM;
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26-MAR-2001; 2001US-00816095.
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Best Local Similarity
Matches 34; Conserva
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                        48.6%; Score 24.8; DB 5; Length 992; 72.7%; Pred. No. 29; ive 0; Mismatches 12; Indels
                                                                                                                                                                                                                            Sequence 992 BP; 273 A; 225 C; 275 G; 218 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                             1 ACAGAACTGGCAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 27787.
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2000US-0189862P.
2000US-0207454P.
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                                                                                                                                                                                                                                                                               Local Similarity
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Matches
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                                                                                                                                                                New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                             The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 116297 BP; 33950 A; 22909 C; 23278 G; 36160 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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70.8%; Pred. No. 41;
ive 0; Mismatches
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                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 564; 199pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monahan JE;
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                  27-DEC-2002; 2002US-00330773.
                                                               (SAGR-) SAGRES DISCOVERY INC.
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 22-DEC-2003; 2003WO-US041389
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                                                                                                Morris DW, Malandro MS;
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                                                                                                                                 WPI; 2004-543781/52
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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16-MAR-2000;
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20000S-0229287P.
20000S-0229343P.
20000S-0229344P.
20000S-0229345P.
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2000US-0246613P.
2000US-0249207P.
                    2000US-0227182P.
2000US-0227009P.
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2000US-0229513P.
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2000US-0241787P.
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                  22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
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14-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
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20-0CT-2000;
10-NOV-2000;
08-NOV-2000;
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25-SEP-2000;
26-SEP-2000;
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13-OCT-2000;
13-OCT-2000;
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17-NOV-2000;
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29-SEP-2000;
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
(f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human musculoskeletal system related polynucleotide SEQ ID NO 3070.
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                                                                                                                                DB 5; Length 992;
                                                                                            Sequence 992 BP; 273 A; 225 C; 275 G; 218 T; 0 U; 1 Other;
                                                                                                                                                                                                                                            624 ACTGCACTGTCAAGGCTGCAAGAGGCTCCTGACGGCTTCTGACA 667
                                                                                                                                                                    12; Indels
                                                                                                                                                                                                        ACAGAACTGGCAAAGAGCAAGAGGTCACTGAGGGCCTCTGTCA 44
                                                                                                                              Query Match
Best Local Similarity 72.7%; Pred. No. 29;
Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0180638P.
24-FEB-2000; 2000US-0180638P.
16-MAR-2000; 2000US-0189133P.
17-MAR-2000; 2000US-0199123P.
18-AFR-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0209123P.
19-MAY-2000; 2000US-020918P.
19-MUS-2000; 2000US-02198129P.
10-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0214896P.
11-JUL-2000; 2000US-021829P.
11-JUL-2000; 2000US-021829P.
14-MUG-2000; 2000US-02218P.
14-MUG-2000; 2000US-022518P.
14-MUG-2000; 2000US-0225214P.
14-MUG-2000; 2000US-0225214P.
14-MUG-2000; 2000US-0225214P.
14-MUG-2000; 2000US-0225266P.
14-MUG-2000; 2000US-0225267P.
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2000US-0226279P.
2000US-0226681P.
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                                                                                                                                                                                                                                                                                                                                   AAL36705 standard; DNA; 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculoskeletal system; ds
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
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The invention relates to novel genes (AAL13669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and disclosed in the specification. The nucleic acids, proteins, antibodies of acids (all) sancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid a ratherfus and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. carebral anoxia and epilepsy; and (f) infectious diseases such as viral, chais patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis.
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Pred. No. 32;
0; Mismatches 11; Indels (
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          17. NOV-2000; 2000US-0249209F.
17. NOV-2000; 2000US-0249210P.
17. NOV-2000; 2000US-0249211P.
17. NOV-2000; 2000US-0249211P.
17. NOV-2000; 2000US-0249214P.
17. NOV-2000; 2000US-0249214P.
17. NOV-2000; 2000US-0249216P.
17. NOV-2000; 2000US-0249216P.
17. NOV-2000; 2000US-0249216P.
17. NOV-2000; 2000US-0249216P.
17. NOV-2000; 2000US-0249218P.
17. NOV-2000; 2000US-0249214P.
17. NOV-2000; 2000US-0249244P.
17. NOV-2000; 2000US-0249244P.
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01-DEC-2000; 2000US-0250391P.

05-DEC-2000; 2000US-0251030P.

05-DEC-2000; 2000US-0251988P.

05-DEC-2000; 2000US-0251988P.

06-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251868P.
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17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
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31; Conservative
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Matches 31; Conserv
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Cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral; antiallergic, hepatotropic, antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                             Human musculoskeletal system related polynucleotide SEQ ID NO 3069.
               AAL36704 standard; DNA; 331 BP
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2000US - 0225513P .
2000US - 0225213P .
2000US - 0225214P .
200US - 022526P .
2000US - 0225268P .
2000US - 025256P .
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2000US-0225758P
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2000US-0226279P.
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                                                                                                                        musculoskeletal system; ds.
                                                (first entry)
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28-JUN-2000;
30-JUN-2000;
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RESULT 15
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08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0232081P.
14-SEP-2000; 2000US-0232081P.
14-SEP-2000; 2000US-023239P.
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23-CCT-2000; 2000US-023933P.
23-CCT-2000; 2000US-023178P.
23-CCT-2000; 2000US-023178P.
23-CCT-2000; 2000US-023188P.
23-CCT-2000; 
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08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246578P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-024652F.
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17-NOV-2000;
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, and cancer allorative to be an autoimmune thyroiditis, cancer allorative colitis, (b) immune disorders e.g. Addison's disease, allorative colitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis.
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2000US-0250391P.
2000US-0251030P.
2000US-0251988P.
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2000US-0251479P.
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2000US-0251869P.
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2000US-0251990P.
2000US-0254097P.
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Job time : 34.0376 secs
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06-DBC-2000;
06-DBC-2000;
08-DBC-2000;
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1 acagaactggcaaagaggca.....aggggctctgtcacccagga
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

	Description	AC138954 Homo sapi	AC012645 Homo Bapi	AC094359 Rattus no	AC128457 Rattus no	AC109240 Mus muscu	AL731678 Mouse DNA	AC158791 Mus muscu	AC091314 Mus muscu	AC109504 Mus muscu	AC132271 Mus muscu	AC131679 Mus muscu	AC094305 Rattus no	AC106528 Rattus no	AC149647 Bos tauru	AC008459 Homo Bapi	AC010459 Homo sapi	AC141543 Rattus no	AC125458 Mus muscu
COLUMNICO	ΩI	AC138954	AC012645	AC094359	AC128457	AC109240	AL731678	AC158791	AC091314	AC109504	AC132271	AC131679	AC094305	AC106528	AC149647	AC008459	AC010459	AC141543	AC125458
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	& Query Match	98.0	98.0	58.0	58.0	54.1	54.1	54.1	54.1	54.1	53.7	53.7	52.2	52.2	52.2	51.4	51.4	51.4	51.4
	Score	50	20	29.6	29.6	27.6	27.6	27.6	27.6	27.6	27.4	27.4	26.6	26.6	26.6	26.2	26.2	26.2	26.2
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RESULT 3
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Submitted (06-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 192943)
Stanford Human Genome Center and Los Alamos National Laboratory.

DOE Joint Genome Institute
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 192943)

1DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Homo sapiens chromosome 16 clone RP11-455F5, complete sequence.
ACO12645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                   1225: contig of 1225 bp in length
1325: gap of unknown length
34247: contig of 32922 bp in
34347: gap of unknown length
71258: contig of 36911 bp in length
71358: gap of unknown length
117554: contig of 46196 bp in length
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5 187383: contig of 69729 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-828420"
/clone lib="RPCI human BAC library 11"
1226. __1325
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117555. .117654
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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DOE Joint Genome Institute.
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Sukaryota; Metazous Chordaea; Craniata; Vertebrata; Euteleostomi; Martus norvegicus sucrepticus; Eucheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Murinae; Rattus.

3 (alrognathi; Murcidea; Murinae; Rattus.

3 (alrognathi; Murcidea; Murcinae; Rattus.

3 (alrognathi; Mabbrooks, R., Amin, A., Angulano, D., Anlen, C., Allen, H., Absbrooks, S., Amin, A., Angulano, D., Anlen, C., Allen, W., Barbrooks, S., Amin, A., Angulano, D., Angaliano, D., Bandernanake, D., Barber, M., Barnstead, M., Benahmed, F., Cardenas, V., Carter, K., Carter, R., Blyth, P., Brown, M., Bryant, N., Bular, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bular, J., Chen, G., Copkell, K., Carderon, E., Cardenas, V., Carter, K., Carter, M., Carter, M., Carter, M., Corkrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dengado, O., Denson, S., Deramo, C., Coyle, M., Cree, A., Dioya, K., Bgan, R., Escotto, M., Egene, C., Evenson, C., Purcill, R., Duval, B., Eaves, K., Eraser, C.M., Gabisi, A., Garte, R., Garde, M., Guerra, W., Gabisi, A., Ganta, R., Garde, M., Garrer, T., Garza, M., Gabisi, A., Ganta, R., Garde, M., Hennandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hodges, M., Honling, B., Howells, S., Hull, S., Hume, J., Idlebird, D., Jackson, A., Jang, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, W., Liu, Y., London, R., Marian, R., Marian, R., Mangum, R., Marian, R., Marian, R., Mangum, R., Marian, R., Marian, R., Mangum, R., Mandul, R., Marian, R., Marian, R., Mangum, R., Mandul, R., Marian, R., Mangum, R., Mandul, R., Marian, R., Mandul, R., Mangum, R., Mandul, 
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Submitted (07-JAN-2004) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Jan 7, 2004 this sequence version replaced gi:19172834.

Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory www-shgc.stanford.edu Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, B.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 192943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC094359.6 GI:30467240
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.0%; Score 50; DB 8; Ler
Best Local Similarity 100.0%; Pred. No. 5.2e-09;
Matches 50; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .192943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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Direct Submission.

Submitted (199-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24942531.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Mithin each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                              Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu.L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu.L.-L., Plopper, F., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R., Relily, B., Railly, M., Ran, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Soctt, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Strong, R., Sutton, R., Svarek, A., Tabor, P., Taylor, C., Steinle, M., Strong, R., Sutton, A., Svarek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Waig, S., Wairren, J., Waldron, L., Walker, B., Wang, J., Wang, C., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wight, D., Wight, R., Willson, R., Warken, R., Wooden, H., Worley, K., Widerhausern, A., Weiss, R., Smith, D.R., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a "working daraft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 236591 bases at least Q40 consensus quality: 235691 bases at least Q30 consensus quality: 239010 bases at least Q30 senting the size: 241077 bases at least Q20 Estimated insert size: 24107522; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
Parks, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
    Okwuonu, G., Olarnpunsagoon, A., Pal, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89596: contig of 89596 bp in length
89696: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: GALI
Center clone name: CH230-3C19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 249737)
Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
2 (bases 1 to 249737)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
JOURNAL
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COMMENT

TITLE

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Sciuropathi, Murbidee; Muridae; Murinae; Kattus.

Sciuropathi, Murbidee; Muridae; Muridae; Kattus.

I (bases 1 to 251990)

Mizny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,

Anjalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Bryant, N., Bulary, E., Barch, F., Blyth, P., Brown, M.,

Bryant, N., Bulary, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Clacko, J., Chavez, D., Chen, G., Coylen, Y., Chen, Z., Chu, J.,

Clacko, J., Chavez, D., Chen, G., Coylen, Y., Chen, Z., Chu, J.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Daraper, H., Dugan-Rocha, Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fraser, C.M., Gablsi, A., Gante, R., Garcia, A., Garrer, M., Gavara, W.,

Gebregeorgis, E., Geer, K., Galil, R., Gardy, M., Guerra, W., Guerra, W.,

Gebregeorgis, E., Geer, K., Galil, R., Gardy, M., Guerra, W.,

Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,

Harvey, Y., Havles, S., Hladun, S.L., Hodgson, A., Hogues, M.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Li, Z., Liu, J.,

Lorensuhewa, L., Loulseged, H., Lozado, R., Johnson, R., Johnson, R.,

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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,

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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,

Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251990 bp DNA linear HTG 10-OCT-:
Rattus norvegicus clone CH230-85E19, *** SEQUENCING IN PROGRESS
***, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29.6; DB 14; Length 249737; Pred. No. 0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222041 ACAGATCTGGCAAAGAGGCCAGAGGTGACTGCCTGCCTGTCTTA 221998
248439: contig of 158743 bp in length 248539: gap of unknown length 249737: contig of 1198 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC128457.2 GI:23267595
HTG: HTGS PHASBI; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                        /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        end sequence:BH307413"
895<u>9</u>7. .89696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                  clone end:Sp6
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.0%;
                                                                                                              1. .249737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 79.5'
Matches 35; Conservative
  89697
248440
248540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC128457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                             misc_feature
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AC128457/c
LOCUS
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                 gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap
                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
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Direct Submission

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 251990)

3 (bases 1 to 251990)

3 Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 22, 2002 this sequence version replaced gi:21909161.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequence and whole genome shorgun sequence reads. Both end sequence
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Naris, S., Nankervis, C., Neal, D., Newton, N., Ngyven, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Ploper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Reilly, B., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Shetty, J., Shvartsbern, K., Sisson, I., Sitter, C.D., Snajs, D., Shetty, J., Shvartsbern, A., Sisson, I., Sitter, C.D., Snajs, D., Steinle, M., Strong, K., Sutton, A., Svaren, R., Svare, A., Tabor, P., Taylor, T. Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Wailson, R., Walter, R., Wailson, R., Willson, Von, V., Wilderhausern, A., Weise, R., Dunn, D., Von, N., Weisek, G. and Gibbs, R.A. Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a "working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 251990)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
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AUTHORS
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JOURNAL
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COMMENT

AUTHORS

TITLE

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207842 ACAGATCTGGCAAAGAGGCCAGAGGTGACTGCCTGCCTGTTA 207799
                          unknown length
of 224856 bp in length
             of 11689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCA 44
                                       gap of unknown length
contig of 4723 bp in length
gap of unknown length
                                                                                unknown length
of 1428 bp in length
unknown length
of 1185 bp in length
                                                                                                                                                                              246732: contig of 1118 bp in length
246832: gap of unknown length
248947: contig of 2115 bp in length
                                                                                                                                       unknown length
of 1133 bp in length
unknown length
                                                                                                                                                                                                                                    B 251990: Contig of 2943 bp in length
Location/Qualifiers
                                                                                                                                     ength
                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
                                                                                                                                                                                                                        249047: gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                   and sequence:BH304395"
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241469. .241568
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246733. .246832
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note="wgs end extension
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gap of unk
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/db_xref="taxon:10116"
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clone_end:Sp6
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           contig
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(3176. .34795
                                                                                                                                        gap of
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:3461. .14737
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37663. .39153
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7847. .69250
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72977. .74360
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31426. .132574
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During sequence assembly data is compared from overlapping clones.
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Eg. Chaese 1 to 189212.

Birren, B. Linton, L., Nuebaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, M. Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camara, J., Cangrojano, A., Chang, J., Chazaro, B., Choepel, Y. Colangelo, M. Collins, S., Collymore, A., Cook, P., Colongelo, M., Collins, S., Collymore, A., Cook, P., Earo, S., Gords, S., Goyete, M., Gard, T., Carad, Pietre, N., India, S., Collymore, A., Cook, P., Brown, A., Karatas, A., Karatas, M., Karatas, M., Karatas, M., Marle, C., Lakocque, K., Landscare, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marchas, C., Macchen, C., Spencer, P., Sanger, Phonen, L., Schauer, S., Schubback, R., Senaco, M., Sanger, Phonen, R., Stepace, S., Schaubeck, R., Stenger, Phonen, R., Stepace, S., Schaubeck, S., Stenger, Macchen, C., Lander, B., Mu, X., Waman, D., Yelle, R., W. J., Wanderson, S., Lander, C., Lander, R., Lander, C., Lander, R., Lander, C., Lander, R., Lander, J., Collymon, R., Macchen, C., Lander, R., Lander, J., Collymon, R., Macchen, C., Lander, R., Lander, J., Collymon, R., Macchen, C., Lander, R., Lander, J., Ramanan, J., Pacchen, M., Macchen, J., Backer, M., Sander, J., Collymon, R., Macchen, J., Macchen, J.,
                                          AC109240 189212 bp DNA linear HTG 28-JUN-2005
Mus musculus chromosome 1 clone RP23-445123 map 1, *** SEQUENCING
AC109240 GI:68268179
                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
(bases 1 to 189212)
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On Jun 28, 2005 this sequence version replaced gi:66841635.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                      HTG; HTGS PHASE2; HTGS FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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Mus musculus chromosome 1, clone RP23-445I23
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                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
                                                                            DEFINITION
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AUTHORS
TITLE
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AUTHORS
RESULT 5
AC109240
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Direct Submission
Submitted (21-DEC-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, Carb. 158, UK. E-mail enquirtses:
Cambridgeshire, Car. uk Clone requests: clonerequest@sanger.ac.uk
On Dec 23, 2002 this sequence version replaced gi:26788084.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
shotgun may have been used to confirm this sequence.
Sequence from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
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Mouse DNA sequence from clone RP23-39H12 on chromosome X, complete
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                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 174728 contig of 174728 bp in length

* 174828 igap of unknown length

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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Center: Broad Institute of MIT and Harvard Center code: WIBR
Web site: http://www.seq.wi.mit.edu Contact: sequence submissions@broad.mit.edu Center project Information Center project name: L20866 Center clone name: 445_I_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-23 Female Mouse BAC" 174729. .174828
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Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

BM:, SHALSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-39H12 is from the RPCT-23 Mouse PAC Library constructed by the group of Pieter de Jong.

Por further details see http://www.chori.org/bacpac/home.htm
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Mus musculus chromosome 1 clone RP23-247C6 map 1, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia;
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 239692)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 1, clone RP23-247C6
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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Location/Qualifiers
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Mus musculus
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3. (Dades 1 to 235924)
Bliven, T. (Wisbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, J., Cooke, P., Cocke, P., Carum, B., Choepel, Y., Collymore, A., Dodge, S., Dooley, K., Dorris, L., Brickson, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Uohnson, R., Lovine, R., Lindlad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclan, C., Macdonald, P., Major, J., Manning, J., Marthews, C., Macdonald, P., Major, J., Manning, J., Manning, V., Mardyn, T., Najor, J., Niguyen, C., Niguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Fhunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stemen, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Lopham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Volya, W., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Samann, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Volaman, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-MAR-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 239692)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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Berren, 320 Charles Street, Cambridge, MA 02141, USA

Barna, W. Baerlen, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barna, W. Baerlen, V. Bloom, T., Boguslawkiy, L., Boukhgalter, B., Cook, A., Cooke, P., Chang, J., Chaepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farcelria, P., FitzGerad, M., Gage, D., Galagan, J., Gard, S., Gord, S., TierGerad, W., Gale, D., Galagan, J., Horton, E., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Norman, C., McCarthy, M., Meldrin, J., Mencus, L., Mihova, T., Matthews, C., Norman, C., Murphy, T., Naylor, J., Micol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Kae, C., Rogov, P., Phunkhang, P., Pierre, M., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, M., Stange-Thoman, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Nujel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Aug 20, 2002 this sequence version replaced gi:14336555.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
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Sequencing vector: plasmaid; n/a; 100% of reads
Chemistry: Dyo-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 239546 bases at least Q30

Consensus quality: 239546 bases at least Q30

Consensus quality: 240147 bases at least Q20

Insert size: 230000; agarose-fp

Insert size: 240594; sum-of-contigs

Quality coverage: 13.7 in Q20 bases; sum-of-contigs
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Research, 320 Charles Street, Cambridge, MA 02141, USA
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC091314 242194 bp DNA linear HTG 20-AUG-2002
Mus musculus clone RP23-57B2, WORKING DRAFT SEQUENCE, 17 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, K., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-APR-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227642 ACAGTGCCAGCGCAGAGGTCGCCAGAGGTCCCCTTTCACAGG 227691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.1%; Score 27.6; DB 14; Length 239692; 72.0%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 6.3;
0; Mismatches 14; Indels
                                                                                                                                                                                                             clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC001314.3 GI:22325114
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-57B2
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                                                                                                                                                                                                                                        .88510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inpublished
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ORGANISM
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57902: gap of 100 bp
72870: contig of 14968 bp in length
72970: contig of 100 bp
89540: contig of 100 bp
162712: contig of 73772 bp in length
162812: gap of 100 bp
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220592: contig of 34691 bp in length
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of 10476 bp in length
4201 bp in length
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gap of
contig
                                                                                                                                                                                                                                                                                                                                                                  vector side:left"
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57803
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72871
72971
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89641
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220593
220693
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Dipublished

Siren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Bordialavki, C., Camporlano, A., Chang, J., Changal, J., Camporlano, Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farzeltano, K., Dewar, K., Diaz, J.S., Paro, S., Farzeltano, R., Goyette, M., Graham, L., Grand-Pierre, N., Grarelta, P., FitzHugh, W., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Karatas, A., Kalls, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Mackernan, K., Marjor, J., Marquis, N., Matthews, C., McCarthy, M., McKernan, K., Mells, C., Lakocque, K., Mihova, T., Norman, C.H., O'Connor, Y., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Raback, M., Kaley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stance, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Wassiliev, H., Sancon, N., Wassiliev, M., N., Wassiliev, M., N., Wassiliev, M., N., Was
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Mus musculus chromosome 13 clone RP23-184C21 map 13, WORKING DRAFT
SEQUENCE, 20 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

54.1%; Score 27.6; DB 14; Length 242194;
Best Local Similarity 78.6%; Pred. No. 6.3;
Matches 33; Conservative 0; Mismatches 9; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106371 TGGCCAACAGCCAAGTAACTGAGGCCCTCTGTCCACCAG 106330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TGGCAAAGAGGCAAGAGTCACTGAGGGGCCTCTGTCACCCAG 49
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Mus musculus chromosome 13, clone RP23-184C21
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ACI09504.5 GI:45430118
HTG; HTGS PHASE1; HTGS_FULLTOP.
Mus musculus (house mouse)
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                                                                               misc_feature
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100 bp of 6670 bp in length

00 bp

of 9572 bp in length

TITLE JOURNAL COMMENT

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gap of 100 bp
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/estimated_leng
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              Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matchews, C., McCarthy, M., Meneus, L., Mihova, T., Menthang, P., Pierre, N., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasawy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasawy, U., Raymond, C., Retta, R., Stere, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Trafanes, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Voa, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                              Submitted (13-MRA-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 13, 2004 this sequence version replaced gi:20389429.
All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                          Erickson, J., Faro, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: 120868

Center clone name: 184 C 21

Center clone name: 184 C 21

Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 192122 bases at least Q40

Consensus quality: 194367 bases at least Q30

Consensus quality: 195058 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 185349; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 7.4 in Q20 bases; agarose-fp
Quality coverage: 6.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
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      Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
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Web site: http://www-seg.wi.mit.edu
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Query Match Best Local Matches 3

gap

DEFINITION ACCESSION

RESULT 10 AC132271

ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                      The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The Clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROD 06-FEB-2004
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24956. .25048
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroldea; Muridae; Murinae; Mus
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Mus musculus BAC clone RP23-33916 from chromosome 5, complete
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hote="Sequence derived from PCR product of genomic 167787. 163801
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Haakenson, W., Haglund, K., Bielicki, L. and Meyer, R.

The sequence of Mus musculus BAC clone RP23-33916

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of the clone. Location/Qualifiers 1. 173029 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION
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                                                                                                                                                                http://genome.wustl.edu
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Wilson, R.
                                                     MAPPING INFORMATION:
                                                                                                                                                                                                                     SOURCE INFORMATION:
restriction digest.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 173029)
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Submitted (09-FBB-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 173029)
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Submitted (26-FEB-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC132271 173029 bp DNA linear ROD 08-MA
Mus musculus BAC clone RP24-338E23 from 5, complete sequence.
AC132271
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On Feb 26, 2005 this sequence version replaced gi:58801841.
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Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                            54.1%; Score 27.6; DB 14; Length 329223; 72.0%; Pred, No. 6.4;
                                                                                                                                                                                                                                                                                                                                                         1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG
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Thomlinson,C., Haglund, K. and Bielicki,L.
The sequence of Mus musculus BAC clone RP24-338E23
Unpublished (2001)
Chases 1 to 173029)
Direct Submission
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Contact: submissions@watson.wustl.edu
------ Summary Statistics
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                                                                                                                                                                                                                                                                                                    0; Mismatches
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166997. .222799
/note="assembly_fragment"
222800. .222899
                                                                                                          /estimated_length=100
222900. .229569
/note="assembly_fragment"
229570. .229669
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Mus musculus
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Wilson, R.K.
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ton 6168. .6368

on 7206. .7312."

on 7206. .7332."

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    7995. .8016

n 8227. .8357

/rpt_family="B4"

8720. .8930
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/rpt_family="RMER15"
12692. .12840
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13636. 13829
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| 1462. .157
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5301. .581

/rpt_family="L1"

570t_family="B4"

5686. .6053

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6168. .6368
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17194. 17300
/rpt_family="Alu"
17404. 17610
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/rpt family="Alu"
23665. .23827
/rpt_family="L2"
                                                                          /rpt_family="MIR"
2980. 3174
/rpt_family="L1"
3779. 3963
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/rpt_family="B4"
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22082. .22205
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    'rpt_family="B4"
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3062. .13245
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212<u>9</u>.
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                                                                                                                                                                                                                                                                                                                                                              Submitted (06-FEB-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 16, 2004 this sequence version replaced gi:22475611.
3 (bases 1 to 198890)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (25-MG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                         Direct Submission
Submitted (16-JAN-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, WO 63108, USA
6 (bases 1 to 198890)
Wilson,R.
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                                                                                                                                                         Submitted (29-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 198890)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE INFORMATION:
The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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Center code: WUGSC
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This sequence is the entire insert of the clone.
Location/Qualifiers
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Contact: submissions@watson.wustl.edu
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/mol_type="genomic DNA"
/db xref="taxon:10090"
                                                                                                       4 (bases 1 to 198890)
McPherson, J.D. and Waterston, R.H.
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47. .120
/rpt family="ID"
297. .460
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Sciucopiacuri, Millians, Millians, Martinas, Marcus.
Sallen, C., Allahn, H., Alabrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allahnooks, S., Amin, A., Anguiano, D.,
Anyalabechi, V., Aoyagi, A., Ayodeji, M., Barnstead, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blaix, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Casaar, H., Center, A.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diyya, K.,
Dragac, H., Dugan-Rocha, S., Denmo, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Plagg, N., Forbes, L., Foster, M., Foster, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27.4; DB 9; Length 198890;
Pred. No. 7.5;
0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11491 CTGCCAAAAAAGCACAAGCTCACTGAGAGCTCTGCCTCAAAGGA 11535
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HTG; HTGS PHASEI; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
/rpt_family="MER1_type"
/rpt_family="MER1_type"
25459. .25611
/rpt_family="Alu"
/-7033. .2731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .36689
family="MER1_type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt family="Alu"
5801. .35859
rpt_family="ERV1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38298. 38494
/rpt_family="ERVK"
38675. 38730
                                                                                                                                                                                                                                                                                                                                 /rpt_faml17-
31735. .31881
/rot_family="B4"
                                                                                                                                                                                                                             29380. .29467
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                 7. .32015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .36998
family="B4"
                                                                                                            27083. .27314
/rpt_family="L1"
28449. .28648
                                                                                                                                                                      /rpt_family="B2"
28678. .28866
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="B2"
2221. .32322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="B4"
                                                                                                                                                                                                                                                                                               family="ID"
                                                                                                                                                                                                                                                                                                                           . .30353
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                                                                                                                                                                                                                                                                                                                  30353
                                                                                                                                                                                                                                                           /rpt_family="}
29938. .30007
                                                                                                                                                                                                                                                                                                                                                                                                                           'rpt_family="F
12016. .32220
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34803. .34851
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Best Local Similarity 75.6%;
Matches 34; Conservative
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priser C.M., Cablai A., Ganta R., Garcia A., Garner, T., Garza M., Priser C.M., Cablai A., Garria R., Garcia A., Garrer, T., Garza M., Harvey, Y. Brulak, D., Garcia A., Handras M., Handlis M., Harting M., Carding M., Margal M., Karpaly S., Kally S., Kally S., Hame, J., Galden, M., Joden, D., Jockson, A., Joden, M., Margal M., Market, C.L., Labor, H., Labornan, B., Johnson, B., Jolivet, A., Karpaly S., Kally S., K
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Unpublished
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TITLE
JOURNAL
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JOURNAL
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Rattus norvegicus clone CH230-40B7, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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ACI06528 4 GI:30580732
HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Burchontoglires; Glires; Rodentia;
Sciurcognathi; Muroidea; Muridae; Murinae; Rattus
1 (bases 1 to 261198)
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Consensus quality: 209782 bases at least Q30 Consensus quality: 212122 bases at least Q20 Estimated insert size: 220755; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 231980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%; Score 26.6; DB 14; Length 2
71.4%; Pred. No. 16;
tive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                      227830: contig of 227830 bp in length 227930: gap of unknown length 229995: contig of 1165 bp in length 229195: gap of unknown length 231980: contig of 2785 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /estimated length=unknown
229096. .229195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /estimated_length=unknown
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clone_end:Sp6"
227831. 227930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end_sequence:BH309839"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BH309836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91004. .91190
/note="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95949. .96064
/note="clone boundary
clone_end:Sp6
site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="CH230-3F23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.2
Best Local Similarity 71.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .1374
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229096
229196
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AC106528/c
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VERSION
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Anyalebechl, N., Aoyagika, P., Myodejika, Bacaba, B. Baden, H. Banaba, D. D., Banabana, D. D., Barana, D. D., Banabana, D. D., Barana, D. D., Banabana, D. D., Barana, D. D., Banabana, D. Cardenas, V., Carter, R., Danaba, C., Burch, P., Barrell, K., Calderon, B., Cardenas, V., Canter, R., Danaba, C., Charo, D., Charo, D., Chavez, D., Charo, G., Chen, R., Chen, T., Canter, M., Canter, M., Canter, M., Charo, D., Dasigado, O., Dannon, S., Barana, C., Chien, M., Charo, C., Charo, D., Dasigado, O., Dannon, S., Barana, C., Chien, M., Charo, C., Charo, C., Charo, D., Char
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35; Conservative
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  Matches
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                                                                                                                                                           RESULT 14
AC149647
                                                                                                                                                                                                                                                                             ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                   Consensus quality: 249514 bases at least Q40
Consensus quality: 251911 bases at least Q30
Consensus quality: 251971 bases at least Q30
Consensus quality: 251574 bases at least Q20
Estimated inser size: 26946; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5789 contig of 5789 bp in length
5790 5889: gap of unknown length
5589 255153: contig of 249264 bp in length
5584 255253: gap of unknown length
5254 256303: contig of 1050 bp in length
6304 257841: contig of 1438 bp in length
7842 257841: contig of 1438 bp in length
7842 259377: contig of 1438 bp in length
7842 259477: contig of 1436 bp in length
7842 259477: contig of 1436 bp in length
7843 259477: gap of unknown length
7844 261988: contig of 1721 bp in length.
7845 26198: contig of 1721 bp in length.
                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                     Center: Baylor College of Medicine Center code: BCM
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|organism="Rattus norvegicus"
|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-40B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /estimated length=unknown 5890. 6946
/note="wgs contig"
complement(243387. 244025)
/note="clone_boundary
clone_end:T7
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257842. .257941
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/estimated_length=unknown
256304. .256403
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                                                                                                                                                                              Center clone name: CH230-40B7
------ Summary Statistics
Assembly program: Atlas 3.0;
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clone_end:T7"
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252740. .255153
                                                                                                                                                             Center project name: GLCS
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3771. .5789
/note="wgs_contig"
5790. .5889
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259378
259478
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  table.
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DB 14; Length 261198;

Score 26.6; I Pred. No. 16;

52.2**%**; 71.4**%**;

Query Match Best Local Similarity

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Gaps
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                                                                                                                                                                           198250: contig of 6959 bp in length
198251 198350: gap of unknown length
198351 203718: contig of 5368 bp in length
03719 20378: gap of unknown length
03819 20340: contig of 5522 bp in length
19841 209440: gap of unknown length
198220: contig of 72880 bp in length
Location/Qualifiers
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182944. .183043
/estimated_length=unknown
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189301. .189400
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71122. 71171
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73348. 107554
/estimated length=34207
123341. 123390
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|44613. 144662
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|45740. 151919
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                                                                                                                      Labracted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 29, 2005 this sequence version replaced gi:50540557.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described in dividual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold's and there may be sequence contigs within a contigue scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
             Direct Submission
Submitted (19-JUN-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Mylor Plaza, Houston, TX 77030, USA (bases 1 to 282320)
Cow Genome Sequencing Consortium.
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Contact: hgsc-help@bcm.tmc.edu
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PRI 04-FEB-2003
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DOB Joint Genome Institute.
Direct Submission
Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 136581)
DOB Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                          2. (Dasses 1 to 136581)
DOE Joint Genome Institute.
DOE Joint Genome Institute.
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-FEB-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA.

On Feb 4, 2003 this sequence version replaced gi:14579681.

On Feb 4, 2003 this sequence version replaced gi:14579681.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

Www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.1.

NOTE: Shatter libraries failed to verify the dinucleotide repeat
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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3558. 5794
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                        ACOO8459 136581 bp DNA linear PRI 04-FEI
Homo sapiens chromosome 5 clone CTC-352D11, complete sequence.
ACOO8459
ACOO8459,7 GI:28201472
                                                                                                                                                                                                                                        Hominidae; Homo.

1 (bases I to 136581)

DOB Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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51.4%; Score 26.2; DB 8;
Best Local Similarity 79.5%; Pred. No. 23;
Matches 31; Conservative 0; Mismatches 8;
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                                                                                                                                                                    Homo sapiens (human)
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                                                              DEFINITION
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19816 CTGGCAGATAAGCAGGAGGCCCCTGGAGGCCTCTGTCAC 19854 Search completed: February 7, 2006, 15:20:44 Job time : 281.097 secs 엄

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Gaps

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8; Indels

7 CTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCAC 45

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Sequence 122934,
Sequence 123028,
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Sequence 123116,
Sequence 123311, Ap
Sequence 15217, Ap
Sequence 15217, Ap
Sequence 15219, A
Sequence 15219, A
Sequence 15220, A
Sequence 15220, A
                                                                                   February 7, 2006, 12:30:54; Search time 10.8591 Seconds (without alignments) 8348.349 Million cell updates/sec
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           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
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US-09-949-016-15222
US-09-949-016-15212
US-09-949-016-15212
US-09-949-016-15212
US-09-949-016-15212
US-09-949-016-15212
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                                                                                                                                                                                                                                                   Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         1303057 seqs, 888780828 residues
                                                                                                                                       US-10-623-108-5_COPY_1186_1236
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                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                   Perfect score:
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US-09-9470E-12234, Application US/09949016
| Patent No. 681239 |
| Patent REPRENCE: CLO01307 |
| CURRENT APPLICATION NUMBER: US/09/949, 016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR PPLICATION NUMBER: 60/241, 755 |
| PRIOR PLING DATE: 2000-10-20 |
| PRIOR APPLICATION NUMBER: 60/237, 768 |
| PRIOR APPLICATION NUMBER: 60/237, 768 |
| PRIOR PATENT NUMBER: 60/237, 768 |
| PATE
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Sequence 3, Application US/09816095
Patent No. 6664084
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/09/816,095
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
ILBNGTH: 99916
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Sequence 8380, Ap
Sequence 416, App
Sequence 4237, App
Sequence 3798, App
Sequence 878, App
Sequence 1187, App
Sequence 1187, App
Sequence 1187, App
Sequence 12979, A
Sequence 187024,
Sequence 187024,
Sequence 187025,
Sequence 187026,
Sequence 187026,
Sequence 12462, A
Sequence 12462, A
Sequence 12462, A
Sequence 12462, A
Sequence 12678,
Sequence 12678,
Sequence 12678, Sequence 12678, Sequence 12678, A
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                                                            US-09-949-016-4237
US-09-949-016-4237
US-09-902-540-3798
US-09-902-540-1187
US-09-949-016-15579
US-09-949-016-15579
US-09-949-016-15579
US-09-949-016-187024
US-09-949-016-187025
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US-09-949-016-158393
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Pred. No. 10;
0; Mismatches
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i_LOCATION: (1)...(99916)
/ OTHER INFORMATION: n = A,T,C or G
US-09-816-095-3
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70.8%;
   1191 3
2022 3
2022 3
2028 2
2737 4221
7035 18551
21593 96878 114793
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Best Local Similarity 70.8
Matches 34; Conservative
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601
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56616
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Sequence 123216, Application US/09949016 Patent No. 6812339
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Best Local Similarity 73.81
Matches 31; Conservative
  ; SEQ ID NO 123122
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-123122
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US-09-949-016-123310
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ORGANISM: Human
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; Sequence 122028, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123028
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US-09-949-016-123122
; Sequence 123122, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VBTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TURE REPREBRICE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR PELING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-00-09-08
; PRIOR FILING DATE: 2000-00-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE FRASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                     Length 601;
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Best Local Similarity 73.8%; Pred. No. 10;
Matches 31; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122934
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                   31; Conservative
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Best Local Similarity
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US-09-949-016-122934
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ORGANISM: Human
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Sequence 123310, Application US/09949016

Sequence 123310, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/0241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 123310
                                                                                                                                                                                                                                                                                                                                                                                            PARLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WIMBER: 00/241,755

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PLIING DATE: 2000-04-04

PRIOR PLIING DATE: 2000-10-03

PRIOR PLIING DATE: 2000-10-03

PRIOR PLIING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 601
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Query Match
47.8%; Score 24.4; DB 3; Length 601;
Best Local Similarity 73.8%; Pred. No. 10;
Matches 31; Conservative 0; Mismatches 11; Indels
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TYPE: DNA
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| Sequence 1089, Application US/09902540
| Patent No. 6833447
| GENERAL INFORMATION:
| APPLICANT: Goldman, Barry S.
| APPLICANT: Slater, Steven C.
| APPLICANT: Misgand, Roger C.
| APPLICANT: Wisgand, Roger C.
| TITLE OF INVENTION: Myxcoccus xanthus Genome Sequences and Uses Thereof
| TITLE OF INVENTION: Wyxcoccus xanthus Genome Sequences and Uses Thereof
| TITLE OF INVENTION: Wyxcoccus xanthus Genome Sequences and Uses Thereof
| TITLE OF INVENTION: Wyxcoccus xanthus Genome Sequences and Uses Thereof
| TITLE OF INVENTION: Wyxcoccus xanthus Genome Sequences and Uses Thereof
| TITLE OF INVENTION WYWBER: 60/217,883
| PRIOR PILING DATE: 2000-07-10
| NUMBER OF SEQ ID NOS: 16825
| SEQ ID NO 1089
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APPLICANT: Goldman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPRESENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: 2001-07-10
FRICA APPLICATION NUMBER: 60/217,883
PRICA PAPLICATION NUMBER: 60/217,883
PRICA PAPLICATION NUMBER: 60/217,883
PRICA PAPLICATION NUMBER: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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47.8%; Score 24.4; DB 3; Length 1023;
Best Local Similarity 68.0%; Pred. No. 11;
Matches 34; Conservative 0; Mismatches 16; Indels 0.
     Length 601;
  Score 24.4; DB 3; Length 6 Pred. No. 10; 0; Mismatches 11; Indels
                                                                                                                                                               Sequence 9591, Application US/09902540; Patent No. 6833447; GENERAL INFORMATION:
Query Match
Best Local Similarity 73.8%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Myxococcus xanthus
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US-09-902-540-9591/c
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RESULT 9

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Sequence 1521/Application US/09949016

Sequence 15217, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAEESEQ for Windows Version 4.0

SEQ ID NO 15217

LENGTH: 32379
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sequence 15218, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

SEQ ID NOS: 207012

SOFTWARE: PRAESEQ for Windows Version 4.0

SEQ ID NO 15218

LENGTH: 32379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 32379;
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Best Local Similarity 73.8%; Pred. No. 23;
Matches 31; Conservative 0; Mismatches 11; Indels
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. Sequence 15219, Application US/09949016

. Patent No. 681233

. GENERAL INFORMATION:
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US-09-949-016-15218
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US-09-949-016-15217
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Query Match
Best Local Similarity 73.8%;
Matches 31; Conservative (
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                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15221
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US-09-949-016-15222
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US-09-94-016-15221/c
| US-09-94-016-15221/c
| Sequence 15221, Application US/09949016
| Sequence 15221, Application US/09949016
| Setent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-15220/c
; Sequence 15220, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 73.8
Matches 31; Conservative
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Best Local Similarity 73.8
Matches 31; Conservative
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US-09-949-016-15220
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LENGTH: 32379
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FARENLA INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-00-04-14

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FaetSEQ for Windows Version 4.0

SEQ ID NO 15222

LENGTH: 32379

TYPE: DNA

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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Pred. No. 23;
0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15221
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Patent No. 6812339
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15223
; LENGTH: 32379
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15223
Query Match
Best Local Similarity 73.8%; Score 24.4; DB 3; Length 32379;
Best Local Similarity 73.8%; Pred. No. 23;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Search completed: February 7, 2006, 15:27:25 Job time : 12.8591 secs

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JOS-10-750-623-34830

Sequence 34830, Application US/10750623

Publication No. US20050287531A1

GENERAL INFORMATION:

APPLICANT: PMI GENOMICS, INC.

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom
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Sequence 4, Appl
Sequence 6, Appli
Sequence 64443, A
Sequence 64443, A
Sequence 84243, A
Sequence 13512, A
Sequence 25067, A
Sequence 25067, A
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Sequence 34830, A
Sequence 20700, A
Sequence 20700, A
Sequence 40559, A
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25067, A
44085, A
44085, A
35306, A
35306, A
3270, Ap
                                                                                                            February 7, 2006, 13:52:58; Search time 22.0694 Seconds (without alignments) 1936.698 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/DSO7_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-750-185-40559

US-10-750-623-40559

US-10-750-623-40559

US-11-121-086-4

US-11-121-086-6

US-11-121-086-45

US-11-121-086-45

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US-10-750-185-35306
US-10-750-623-35306
US-11-136-527-3270
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 454, App
Sequence 124, App
Sequence 12, Appl
Sequence 317, Appl
Sequence 3177, Appl
Sequence 40067, A
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Sequence 4067, A
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Sequence 17535, A
Sequence 58686, A
Sequence 58686, A
Sequence 13235, A
Sequence 13235, A
Sequence 13235, A
Sequence 27296, A
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| Sequence 34830, Application US/10750185
| Publication No. US2050260603A1
| GENERAL INFORMATION:
| APPLICANT: DENOMICS, INC.
| APPLICANT: REER, Richard
| APPLICANT: HOLM, Tom
| APPLICANT: BATES, Stephen
| APPLICANT: MAINING STEPHEND
| APPLICANT: PANTIN, Dennis
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| CURRENT FILING DATE: 2003-12-31
| PRIOR APPLICATION NUMBER: US 60/437,482
| PRIOR PILING DATE: 2002-12-31
| NUMBER OF SEQ ID NOS: 64922
| SOFTWARE: PARCELIN VETSION 3.1
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US-10-750-185-5868
US-10-750-185-5868
US-110-750-623-58686
US-110-00-688-130
US-10-995-561-13235
US-10-750-185-27296
                                                                                                                 US-11-136-527-4012
US-10-750-185-40067
US-10-750-623-40067
US-10-750-185-36898
US-10-750-623-36898
                                                                                  US-11-124-368A-3177
US-11-000-688-586
                                                                                                                                                                                                                                                                                                                   US-10-750-623-27296
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; ORGANISM: Bovine 19866880752334
US-10-750-185-34830
 43.9 6215
43.9 36215
43.9 159146
43.9 215308
43.5 221
43.5 201
43.1 1218
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FILE REFERENCE: MMI1100-1
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  APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INPERRING BOVINE TRAITS
FILE REFERENCE: WAILINO-1.
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2004-12-31
PRIORE FILING DATE: 2004-12-31
PRIMER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VEXBION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20700, Application US/10750185
; Sequence 20700, Application US/10750185
; Publication No. US2050260603A1
; GENERAL INPORMATION:
    APPLICANT: MIGENOMICS, INC.
; APPLICANT: KERR, Richard
; APPLICANT: KERR, Richard
; APPLICANT: ROBINELD, David
; APPLICANT: BATES, Stephen
; APPLICANT: BATES, Stephen
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIM, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR PILING DATE: 2002-12-31
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47.5%; Score 24.2; DB 7; Length 1656;
Best Local Similarity 71.1%; Pred. No. 7.9;
Matches 32; Conservative 0; Mismatches 13; Indels 0
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Pred. No. 11;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 AACAGTCAGTGAGAATAGAGATCGAAGAGGCTCTGCCACCCAG 622
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; Sequence 20700, Application US/10750623
; Publication No. US20050287531A1
; APPLICANT: MAI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERK, Richard
; APPLICANT: RERK, Richard
; APPLICANT: HOLM, Tom.
                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bovine 19866880752334
US-10-750-623-34830
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Best Local Similarity 76.3%;
Matches 29; Conservative (
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 20700
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US-10-750-185-20700
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US-10-750-185-20700
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US-10-750-623-20700
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LENGTH: 1656
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APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Demnis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MM11100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
46.3%; Score 23.6; DB 7; Length 903;
Best Local Similarity 76.3%; Pred. No. 12;
Matches 29; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                              DB 7; Length 600;
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46.3%; Score 23.6; D
Best Local Similarity 76.3%; Pred. No. 11;
Matches 29; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 20700
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40559, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40559, Application US/10750623
Publication No. US20050287531A1
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, ORGANISM: Bovine 19866881097008
US-10-750-185-40559
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APPLICANT: WMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Bovine MMBT20675
US-10-750-623-20700
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Gaps

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Indels

13;

DB 7; Length 34875;

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45.5%;
                                            Query Match
Best Local Similarity 70.5
Matches 31; Conservative
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US-10-750-185-64443/c
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US-11-121-086-4/c
US-10-775-169-316
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APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: Way Luke
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FRIOR PAPLICATION NUMBER: US 60/568,845
FRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SEQ ID NO 3178
LENGTH: 201
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APPLICANT: Wyeth
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REPERENCE: AM10.1080 (031896-01300)
CURRENT APPLICATION NUMBER: US/10/775,169
VORRENT PILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 8278
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 AAACAATTTTCAGGGAGTCRTGAAGCCCTTCTGGGCCTCTTCCACCAGGA 70
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                                                                                                                                                                                                                             DB 7; Length 903;
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                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.4; DB 8; Length 2 Pred. No. 10; 1; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                1 ACAGAACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCT 38
                                                                                                                                                                                                                         Score 23.6; DE Pred. No. 12; 0; Mismatches
    PRIOR APPLICATION NUMBER: US 60/437,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3178, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
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; Sequence 316, Application US/10775169
; Publication No. US22050287532A9
; GENERAL INFORMATION:
                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bovine 19866881097008
US-10-750-623-40559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%;
                     PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 40559
LENGTH: 903
                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.3%;
Matches 29; Conservative
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Best Local Similarity 64.79
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ORGANISM: Homo sapiens
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US-11-124-368A-3178/c
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ORGANISM: Homo
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LENGTH: 34875
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; Sequence 6, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INPORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: POULSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2005-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LINGTH: 172543
                                                                                                                                                                                                                                           Sequence 4, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTY.

FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT APPLICATION NUMBER: 05/574

FILE REFERENCE: 09138.600-00000

CURRENT FILING DATE: 2005-05-04

PRIOR FILING DATE: 2005-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3

SEQ ID NO 4

LENGTH: 164810
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                                                                                                                          Score 23.2; DB 8; Length 1
Pred. No. 48;
0; Mismatches 13; Indels
                                                                                           7 CTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAGG 50
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Score 23.2; DB Pred. No. 35; 0; Mismatches
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Best Local Similarity 70.5%;
Matches 31; Conservative
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CORGANISM: Homo sapiens
US-11-121-086-4
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ORGANISM: Homo sapiens
US-11-121-086-6
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Matches
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US-10-750-623-64443/c
| Sequence 64443, Application US/10750623
| Sequence 64443, Application US/10750623
| Publication No. US20050287531A1
| GENERAL INFORMATION:
| APPLICANT: MIGROWICS, INC.
| APPLICANT: RERR, Richard
| APPLICANT: RERR, Richard
| APPLICANT: HOLM, Tom
| APPLICANT: BATES, Stephen
| APPLICANT: FANTIN, Dennis
| APPLICANT: FANTIN, Dennis
| TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
| FILE REFERENCE: MATIN 0-1
| CURRENT APPLICATION NUMBER: US/10/750,623
| CURRENT FILING DATE: 2003-12-31
| PRIOR FILING DATE: 2002-12-31
| NUMBER OF SEQ ID NOS: 64922
| SOFTWARE: PALENTIN version 3.1
| LENGTH: 944
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Sequence 64443, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, INC.
APPLICANT: RERR, Richard
APPLICANT: RERR, Richard
APPLICANT: RESENGENCE.
APPLICANT: RATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FATES, Stephen
APPLICANT: FATES, Stephen
APPLICANT: FATES, Stephen
APPLICANT: PRINTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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Best Local Similarity 68.1%; Pred. No. 20;
Matches 32; Conservative 0; Mismatches 15; Indels
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; Publication No. US20050272054Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Bovine 19866881015183
US-10-750-623-64443
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US-10-750-185-64443
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 64922
SOFWARE: Patentin version 3.1
SEQ ID NO 64443
LENGTH: 944
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Matches 32, Conservative
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US-10-995-561-84242
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FEATURE:
NAMEKEY: misc feature
LOCATION: (1)...(40000)
LOCATION: (1)...(40000)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2 US-10-995-561-13512
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLSS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILEM DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASESE for Windows Version 4.0
SEQ ID NO 84242
LENGTH: 201
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TYPPF. ....
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER: QC SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 45
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44.7%; Score 22.8; DB 7; Length 40000;
Best Local Similarity 68.2%; Pred. No. 50;
Matches 30; Conservative 1; Mismatches 13; Indels 0;
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; Sequence 1352...
; Sequence 13 No. US20050272054A1
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: BETECTION AND USES THEREOF;
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FESTESEQ for Windows Version 4.0
; SEQ ID NO 13512
; LENGTH: 40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ACTGGCAAAGAGGCAAGAGGTCACTGAGGGCCTCTGTCACCCAG 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Conservative
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CORGANISM: Homo sapiens
US-10-995-561-84242
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-995-561-13512
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; LENGTH: 182303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-45
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Search completed: February 7, 2006, 14:11:06 Job time : 22.0694 secs

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ö Query Match 44.7%; Score 22.8; DB 8; Length 182303; Best Local Similarity 66.0%; Pred. No. 68; Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps ò

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Thu Feb

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OM nucleic - nucleic search, using sw model

Pebruary 7, 2006, 12:27:59 ; Search time 9908.9 Seconds
(without alignments)
10538.142 Million cell updates/sec Run on:

US-10-623-108-5 1837 Title: Perfect score:

1 gaggagtggagatggcggcg.....tagagatgtgtctatggctg 1837

Sequence:

5883141 seqs, 28421725653 residues Searched:

IDENTITY NUC Gapox 1.0

Scoring table:

11766282 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database

90 ba: *
90 in: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		AR164078 Sequence	BD058089 Antibense	CS063502 Sequence	CS081283 Sequence	AX770530 Sequence	X60188 Human ERK1	AX676347 Sequence	M84490 Human extra	AK091009 Homo sapi	BX537897 Homo sapi	Z11696 H.sapiens 4	AY888192 Synthetic	AY890458 Synthetic	AY893270 Synthetic	AX722274 Sequence	AY335595 Synthetic	AY890764 Synthetic
SUMMARIES	ID	BC013992	AR164078	8085009	CS063502	CS081283	AX770530	HSERK1	AX676347	HUMKER1A	AK091009	HSM806004	HS44KDAP	AY888192	AY890458	AY893270	AX722274	AY335595	AY890764
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	Query Match Length DB	1813	1866	1866	1866	1866	1866	1866	3732	1745	2567	2722	1284	1140	1140	1140	1140	1140	1140
de	Query Match	93.9	93.0	93.0	93.0	93.0	93.0	93.0	93.0	88.8	84.2	83.9	65.4	62.1	62.1	62.1	62.0	62.0	62.0
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AY890765 A84423 BD082524 BD228337	CQ829947 AR279902 AX427322 AX803349 BC029712	S46779 RATERKIA RNU12008 MMERKI	KATEKKI ARO16531 ARO36244 ARI71290 ARI72791 I34199	AY033607 RNMAPKIN A84441 BD082533 CQ8229915 AR279911 AX427340
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19 20 21 22	23 25 26 27	28 30 31		8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

	BC013992 1813 bp mRNA linear PRI 29-JUN-2004	Homo sapiens mitogen-activated protein kinase 3, mRNA (cDNA clone MGC:20180 IMAGE:3634492), complete cds.	BC013992	BC013992.1 GI:15559270		Homo Baptens (numan)	Eukarvota: Metazoa;	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	Hominidae; Homo.	1 (Dates 1 to 1015)	Strausberg, K.L., Felligold, B.A., Glouse, L.M., Darge, C.S.,	Altachil S.F. Zeeberg B. Buetow.K.H., Schaefer.C.F., Bhat, N.K.,	Hopkins R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,	Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,	Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,	Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,	McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,	Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, K.A.,	Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,	Sanchez, A., Whiting, M., Madah, J., Young, A.C., Shevuelko, I.,	BOULTAIN G.G., BlakeBley, K.W., IOUCIMIAIO. G.C., GLOWINE B.W.	DICKBOLL R.C., KOULLSUGER, A.C., GILLWOOD, D., DOLLWOOD, D., T. C., T. C., C. C., C.,	BUTCELIBIALY: 13.5., ALZymilar, m.1., Sharasha, o., Guitaria, m.1., Sharasha, o., Gribain I E Johnes X I and Marra M.A.	Scinision, 300 cmc11, 001.00 cmc3, 200 cmc3, 200 cmc11. length	human and mouse cDNA sequences	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	12477932	2 (bases 1 to 1813)	Strausberg, R.	Direct Submission	Submitted (10-588-2001) National Institutes of Meatin, Mammaran. Gene Collection (MGC), Cancer Genomics Office, National Cancer	
RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			KEFEKENCE	AUTHORS																T.T.T.T.		JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG
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                                                                                                                                                          Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupte,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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                                                                                                                                                                                                                                                                                                                                               clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAL Plate: 28 Row: d Column: 11 htts clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
     Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGAGTGGAGATGGCGGCGGCGGCGCCTCAGGGGGGCGGGGGGCGGGGGAGCCCCGTAGAA
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                                                  Contact: MGC help desk famil: Gapbs.remail.nih.gov. Trissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Rubin Laboratory Constitution Rubin Laboratory DNA Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC).
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/protein id="AAH13992.1"
/db_xref="G1:15559271"
/db_xref="GeneID:5595"
/db_xref="GeneID:5595"
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/note="synonyms: P44ERK1, P44MAPK, ERK1,
/db_xref="GeneID:5595"
/db_xref="MIM:601795"
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//db_xref="texon:9606"
/db_cref="texon:9606"
/clone="MGC:20180 IMAGB:3634492"
/tissue type="Lymph, Burkitt lymphoma"
/clone lib="MH MGC 8"
/lab host="BH10B-R"
/note="Vector: pOTB7"
                                      URL: http://mgc.nci.nih.gov
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Pred. No. 8.6e-293;
0; Mismatches 0;
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/organism="Homo sapiens"
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/codon_start=1
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                                                                                                                                            Gaps
                                                                                                                                           54;
                                                                                                               Length 1866;
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                                                                                                                .9 EC
Location/Qualifiers.
Location/Qualifiers
                                                                                                             Score 1708.4; DB
Pred. No. 7e-290;
0; Mismatches

    .1866
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

                                                                                                                Query Match 93.0%;
Best Local Similarity 97.0%;
Matches 1783; Conservative (
     Key
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E 1 (bases 1 to 1866)
S Sivaraman, V.S., Wang, H.Y. and Malbon, C.C.
Antisense oligonucleotides for mitogen-activated protein kinases as thereapy for breast cancer
Lherapy for breast cancer
Patent: JP 200151881-A 1 16-OCT-2001;
FHE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
OS Homo sapiens (human)
PP 19-00151881-A/1
PD 16-OCT-2001
PP 19-MAR-1998 UP 1998541700
PI VIMALA S SIVARAMAN, MSIEN YU WANG, CRAIG C MALBON PC
C12N15/11, A61K31/70, C12Q1/68/A61K48/00
CC The molecular type is CDNA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                 Munnes, M. and Bojar, H.
Methods and kits for investigating ca
Patent: EP 1522594-A 486 13-APR-2005;
Bayer HealthCare AG (DE)
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    1866
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
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LOCUS DEFINITION Sequence 486 from Patent WO2005040414. ACCESSION CS081283. VERSION CS081283. VERSION CS081283. VERSION CS081283.  C	Query Match         93.0%;         Score 1708.4;         DB 6;         Length 1866;           Best Local Similarity         97.0%;         Pred. No. 7e-290;         Anatches 1783;         Conservative         0;         Mismatches         1;         Indels 54;         Gaps         2           Qy         3 GGAGTGGAGGTGGCGGCGGCGGCGGGGGGGGGGGGGGGG	Qy         63 GAGGGGGTCCGGGGGGAGGTGGAGATGCTGAAGGGCAGCCGTTCGAC         122           Db         124 GAGGGGTCGGCGGGGGGGGGGGAGGTGGTGAAGGGGCAGCCGTTCGAC         183           Qy         123 GTGGGCCGGCGTTACAGGCGTTACATGCAGTACATCGGCGGTACGGCGTACGGCATGCTCAGC         182           Db         184 GTGGGCCGGCGTACACGCAGTTGCAGTACATCGGCGAGGCGCGTACGGCATGGTCAGC         243	Qy         183 TCGGCCTATGACCACGTGGCAAGACTCCGTGGCCCATCAAGAAGATCAGCCCCTTCGAA         242           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         303 GAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGGAT 362           Db         364 GAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAGAT 423           Qy         363 GTCTACATTGTGCAGGACCTGATGGAGACTGACAGTTGCTGAAAGCCAGCAGAGAGCAGAGAGAG	423 CTGAGCAATGACCATATCTGCTACTTCCTCTGCGGATCCTGCGGGGGCCTCAAGTACATC	Db 544 CACTCCGCCAACGIGCTCCACCGAGAICIAAAGCCCTCCAACCIGCTCAGCAACACCAC 503  Qy 543 TGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACCAC  Db 604 TGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACCAC 663	Qy         603 ACCGGCTTCCTGACGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGCTG         662           b         664 ACCGGCTTCCTGACGGAGTATGTGGCTACGGGCTCCGGGCCCCCAGAGATCATGCTG         723           Qy         663 AACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTGAG         722           Db         724 AACTCCAAGGGCTATAACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTGAGTGAG
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Oy 1800 CCGTCTAATATAAATATAGAGATGTCTATGGCTG 1837 	6 AX770530 TION Sequence 36 F ION AX770530 N AX770530.1 G DS	SOURCE Homo sapiens (Tuman) ORGANISM Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini; Hominidae: Homo	REFERENCE 1 AUTHORS Munnes, M., Gehrmann, M., Wick, M. and Schmitz, G. TITLE Genes and proteins for prevention, prediction, prognosis and TITLE therapy of Cardiovascular disease	JOURNAL Patent: WO 03031650-A 36 17-APR-2003; Bayer Aktiengesellschaft (DE) FEATURES Location/Qualifiers 1. 1866		Query Match Query Match Query Match Best Local Similarity 97.0%; Pred: No. 76-290; Matches 1783; Conservative 0; Mismatches 1; Indels 54; Gaps 2;	ATGCCGCCGCCGCCCCCTA ATGCCGCCGCCGCCCCCTAAGGGGGGGGGG	Н	Oy 123 GTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGGGGGTACGGCATGGTCAGC 182	183	Oy 243 CATCAGACCTACTGCCAGGGCACGCTCCGGGAGATCCTGCTGCTGCTGCTTCCGCCAT 302	Oy 303 GAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCTGGAAGCCATGAGAGAT 362	363 424	48 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Oy 483 CACTCGGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACGTGCTCATCAACACCACC 542	Oy 543 TGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGAGCGC 602
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                                                                                                                                                                                                                                                                                                                                  Score 1708.4; DB 6; Length 3732;
Pred. No. 6.5e-290;
0; Mismatches 1; Indels 54;
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73._.1212
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llarity 97.0%;
Conservative (
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tches 1783;
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361 AAAAGCCAGCAGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGC
                        CTCAAGTACATCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTC
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1 (bases I to 1745)

Owaki, H., Makar, R., Boulton, T.G., Cobb, M.H. and Geppert, T.D.

Extracellular signal-regulated kinases in T cells: characterization of human ERK1 and ERK2 cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="PRRTEGYCPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVS
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GCILAEMLSNRPIPFEKHYLDQLMHIGILGSPSQEDLINCIINMKARNYLQEDSKTK
VAMAKLFPKSDSKALDLLDRMLTFNPWRRITVERALAHPYLEQYYDFTDEPVAEEFFT
                            PRI 27-APR-1993
3' end.
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                                                                                                                                                                                                                Biophys. Res. Commun. 182 (3), 1416-1422 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1745;
                            HUMKERIA 1745 bp mRNA linear
Human extracellular signal-regulated kinase 1 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1632; DB 8; Length 1
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0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="T_CELL"
/cell_type="CEM_CELL_LINE"
1. 1745
                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
/product="kinase 1"
/protein_id="AAA36142.1"
/db_xref="GI:186696"
                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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1. .1745
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llarity 96.7%;
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Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Mashi, Y., Nagai, K. and Isogai, T.  TITLE NEDO human cDNA sequencing project Unpublished Jeases 1 to 2567)  RESOGAI, T. and Yamamoto, J.  TITLE SUbmitted (04-UTL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7  Kazusa-Kamatari, Kisarau, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  Kazusa-Kamatari, Kisarau, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  COMMENT  Research Helix Research Institute (HRI) insert sequencing: Research Association for Biotechnology (RAB); cDNA library Construction: Helix Research Institute of Technology and Byaluation; Clone selection for full insert sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; Clone selection for full insert sequencing: RAB, RAB, RAB, RAB, RAB, RAB, RAB, RAB,	IGIN Query M Best Lo Matches	
Qy         1551 GAGGGTGGGGGGGGGGGTTAGGGGCCATGCCTGCCCCCCCTCATCTCATTCAA         1610           Db         1448 GAGGGTGGGGGGGGTGAGTAGGGACTCAGGGCCATGCCTCCCTC	AKO91009 AKO91009 AKO91009 AKO91009 AKO91009 AKO91009 DEFINITION HOWO SADPIGNED STATA93690 (fis, clone BRAWH2002967, highly similar ACCESSION AKO91009. AKO91009.1 GI:21749281 AMMMANIA AKOMANIA AKO	GGCO, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watenabe, K., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Takurata, S., Fukuzuni, Y., Pujimori, Y., Komiyama, M., Tachiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noquchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumra, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Nakagawa, K., Okumura, K., Oyama, M., Hata, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs nat. Genet. 36 (1), 40-45 (2004)  REFERENCE 2  REFERENCE 2  AUTHONS (Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K.,

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Fobo, G., Han, M. and Wiemann, S.

Direct Submission

Direct Submission

Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;

sequenced by BMFZ (Biomedical Research Center at the

Heinrich-Heine-University, Duesseldorf/Germany) within the CDNA

sequencing consortium of the German Genome Project. This clone

(DKF2D68600215) is available at the RZPD in Berlin. Please contact

the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available

at http://mips.gsf.de/proj/CDNA/.
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/tissue type="human cervix"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
/dev Betage="adult"
<1. .2722
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                                                                                                           HSM806004 2722 bp mRNA linear PRI 17-APR-2005
Homo sapiens mRNA; cDNA DKFZp68600215 (from clone DKFZp68600215).
BX537897
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase 3, N-terminus
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Pred. No. 1.8e-260;
0; Mismatches 7;
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/mol_type="mRNA"
/db_xref="RZPD:DKFZp68600215"
/map="l6"
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1 (bases 1 to 2722)
Koehrer,K., Beyer,A., Mewes,H., Fobo,G., Han,M. and Wiemann,S.
                                                                                                                                                                                                                                                         BX537897.1 GI:31873912
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Matches 1606; Conservative
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Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This CDS clone is a perated by Harvard Institute of Proteomics. This CDS clone has been cloned by Harvard Institute of Proteomics. This ORP clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-bual vector. Additional sequences in the clone: 'ACC' after Sall site and
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other sequences, artificial sequences.

1 (bases 1 to 1140)
Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Williamson,J. and LaBaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
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Human ORF Project.

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other sequences; artificial sequences.

1 (bases 1 to 1140)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.

Cloning of human full-length CDS in Creator (TM) recombinational
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SKGYTKSIDIWSCGCILAEMLSNRPIPPGKHYLDQLMHILGILGSPSQEDLNCIINMK
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VTG' to provide Kozak consensus sequence. Is isolated and full-length sequence-verified. Location/Qualifiers
                                                                                                       /organism="synthetic construct"
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/gene="MAPK3"
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Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J. Direct Submission

L. Direct Submission

Cambridge, MA 02141, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length
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/note="derived from Homo sapiens first strand cDNA library
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                                                                                                                                                                                                              CTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCCAAGCTTTTCCCCCAAGTCAGAC
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1 (bases 1 to 1140)
Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and Labaer, J. Cloning of human full-length CDS FLEXGene in Gateway (TM) recombinational vector system
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LQYIGEGARVSAXDHYKRRVAIRXISPERALOTYCQFTLERIQILARFRHENVIG
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SKGYTKSIDINSVGCILABMLGNRPIPPEKHYLDQLNHIGILGSPSQBDLNCIINMK
ARNYLQSLPSKTKVANAKLPRSDSKALDLLDRMLTPRPNKRITVBEALAHPYLEQYY
DPTDEPVAERPPREALANDLUDENKLTRPKEQYY
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                     Copyright
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OM nucleic - nucleic search, using sw model

7, 2006, 12:22:44; Search time 1117.96 Seconds (without alignments) 10951.209 Million cell updates/sec February Run on:

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1 gaggagtggagatggcggcg......tagagatgtgtctatggctg 1837 Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

9993994 Total number of hits satisfying chosen parameters: 4996997 seqs, 3332346308 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STRAMMER

SUMMAKIES	DB ID Description	14 ADW12904 Human SMA		2 AAV62478 Aav62478 Human MAP	6 ABK84604 Human cDN	8 ACA89915 Aca89915 Gene diff	12 ADO24424 Human PRO	14 ADZ10042 Human bre	6 ABK90802 DNA encod	9	4 AAI59696 Human pol	4 AAI57910 Aai57910 Human pol	14 ADW12902 Human SMA	14 ADW12900 Human SMA	12 ADH48413 Adh48413 Human KPP	10 ADH59631 Erkl enco	2 AAV71022 Erkl-gree	3 AAD00036 BGFP-Erk1	13 ACN41199 Human dia	
	* Duery Match Length DB	1837	1813	1866	1866	1866	1866	1866	3732	1777	1868	1869	1726	1654	1699	1140	1896	1896	1305	
	Query Match	100.0	93.9	93.0	93.0	93.0	93.0	93.0	93.0	92.9	92.2	91.4	8.98	79.0	78.2	62.0	62.0	62.0	61.4	
	Score	1837	1725	1708.4	1708.4	1708.4	1708.4	1708.4	1708.4	1707	1694	1679.8	1595	1451	1437	1138.4	1138.4	1138.4	1128	
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Abz77131 Human pro	Aac99095 Human pan	Aba96212 Extracell	Adx26048 Novel cel	Abx72224 Human NOV	Aag20260 ERK1. 8/2	Acn41201 Human dia	Acn41202 Human dia	Adv41142 Rat cardi	Adx26182 Novel cel	Aav71030 Erk1-gree	Acn41203 Human dia	Adg86026 Human tum	Adp56267 Human PRO	Ad892937 Mitogen-a	Ady15945 DNA encod	Aav62479 Human MAP	Abl59534 Human mit	Abk90803 DNA encod	Acf12891 Human cer	Ady20280 DNA encod	Adf81745 Leukaemia	Abk84759 Human cDN	Aca56665 Human sig	Adi56461 Human pol	Adv42655 Human psy
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20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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DNA purification; diagnosis; cancer; mitogen-activated protein kinase;
                                                                                                 Location/Qualifiers
12. .1151
/*tag= a
/product= "SMAPK3V3 protein"
       ADW12904
ID ADW12904 standard; cDNA; 1837 BP.
                                                                                                                                                                          18-JUL-2003; 2003US-00623108.
                                                                                                                                                             18-JUL-2003; 2003US-00623108.
                                                     Human SMAPK3V3 variant gene.
                                       (first entry)
                                                                                                                                                                                                                 WPI; 2005-080923/09.
                                                                                                                                                                                                                        P-PSDB; ADW12905
                                                                                                                                   US2005013817-A1.
                                                                                                                                                                                        (DAIK/) DAI K.
                                                                                      Homo sapiens
                                       07-APR-2005
                                                                                                                                                20-JAN-2005.
                                                                         gene; ss.
                          ADW12904;
                                                                                                                                                                                                    Dai K;
                                                                                                   Key
RESULT 1
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Claim 4; SEQ ID NO 5; 55pp; English.

The invention relates to novel isolated polypeptide (I) comprising an

New isolated SMAPK3 polypeptides and nucleic acids, useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal.

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amino acid sequence selected from sequences comprising 335 or 359 amino acids (ADM12901 or ADM12903) or its fragments. The polypeptides and polymuclectides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal. The fragments of the polypeptides and polymuclectides can also be used as primers or probes. This sequence corresponds to the cDNA encoding the SMAPK3V1 variant protein.
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 1813;
                 Systemic inflammatory response syndrome; SIRS; antibacterial; immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
                                                                                                                                                                                                                                                                                                                                        Sequence 1813 BP; 380 A; 580 C; 510 G; 343 T; 0 U; 0 Other;
                                                                                                                              Zipfel PF,
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     Human SIRS/sepsis diagnostic marker DNA fragment 6266.
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Pred. No. 0;
0; Mismatches
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                                                                                                                              'n,
                                                                                                                              Saluz
                                                                                                                                                                                 Disclosure; Page; 75pp; German
                                                                                       02-APR-2003; 2003DE-01015031.
08-AUG-2003; 2003DE-01036511.
02-SEP-2003; 2003DE-01040395.
                                                                                                                                                                                                                                                                                                                        indexing
                                                                          31-MAR-2004; 2004WO-EP003419
                                                                                                                                                                                                                                                                                                                                                      Query Match 93.9%;
Best Local Similarity 97.2%;
Matches 1786; Conservative
                                                                                                                              Reinhart K,
                                                                                                                 (SIRS-) SIRS LAB GMBH
                                                                                                                                          WPI; 2004-748070/73.
                                                                                                                                                                                                                                                                                                                       account during
                                                 WO2004087949-A2
                                     Homo sapiens
                                                                                                                              Russwurm S,
                                                              14-0CT-2004
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241 AACATCAGACCTACTGCCAGCGCCCCGGGAGATCCAGATCCTGCTGCTGCTTCCGCC
                                                          ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAG
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This represents the cDNA sequence of the human ERK-1, a mitogen-activated protein (MAP) kinase. The invention provides a method of inhibiting malignant neoplastic growth of epithelial or endothelial cell in a mammal which comprises administering to the mammal an effective amount of an oligonucleotide complementary to part of the mRNA for the MAP kinases, ERK-1 or ERK2 which is over-expressed in the mammal. Also provided is a method for identifying and monitoring potentially malignant neoplastic cells by measuring the levels of ERK1 and ERK2 mRNA in epithelial or endothelial cells and comparing it to the levels from normal cells of the same origin. Administration of the ERK1 and ERK2 antisense oligonucleotides (AAV62480 and AAV62481) to neoplastic endothelial or epithelial and endothelial malignancies including primary or metastatic cancers of e.g. the breast, prostate, other endocrine
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Best Local Similarity 97.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 54;
                                                                                                                                                                                                                                                                                                  Sequence 1866 BP; 380 A; 605 C; 535 G; 346 T; 0 U; 0 Other;
activating protein kinases ERK1 and ERK2
                               Disclosure; Page 11-12; 59pp; English.
                                                                                                                                                                                                                                                                          tissue or angiosarcoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERK-1; ERK-2; mitogen-activated protein kinase; MAP kinase; human; inhibition; malignant; neoplastic growth; epithelial cell; mammal; endothelial cell; antisense oligonucleotide; primary cancer; metastatic cancer; brast cancer; prostate cancer; angiosarcoma; endocrine tissue cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG 1786
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01-APR-1997;
12-AUG-1997;
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ABK84604 standard; cDNA; 1866 RESULT

ABK84604;

14-AUG-2002 (first entry)

disease; Human cDNA differentially expressed in granulocytic cells #1175. Human; 88; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; eterile inflammatory disease; psoriasis; rheumatoid arthritis; alomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2

11-APR-2002

03-OCT-2001; 2001WO-US030821

03-OCT-2000; 2000US-0237189P

(GENE-) GENE LOGIC INC.

Vockley ŝ Yamaga Beazer-Barclay Y, Weissman SM,

<u>ب</u>

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 1175; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by (GCA), by detecting the level of expression of gene (s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the CC expression level to an expression level in an unactivated GC, where cd ifferential expression of Gs is indicative of GCA. Also included are differential expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a crisume, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) in a cample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation and agent that modulates the expression of gene(s) from Gs in the tissue. M1 correcting GCA, M2 is useful for detecting an inflammation with an inflammation in a tissue, M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile corresponse of a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse in a subject to a pathogen or sterile corresponse of a subject to a pathogen or sterile inflammation in a tissue, M4 is useful for detecting an A 4604

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                                                                                                                                                                                        disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, conditions and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent ont form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                 Gaps
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Best Local Similarity 97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of predicting, diagnosing or prognosing a cardiovascular disease by detection of a polynuclectide in a biological ample comprises hybridising at least one of the polynucleotide to a nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex. The polynucleotides, polypeptides, antisense molecule, antibody and reagent are useful for preparing compositions for preventing, predicting or diagnosing, or a medicament for treating a cardiovascular disease, e.g. arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction. This sequence represents a gene identified in the invention a being differentially regulated in individuals with cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGGGTCGCCCGGGGGTCCCCGGGGGAGGTGGAGATGGTGAAGGGCAGCCGTTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCGAA
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                                                        pectoris;
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                                                     Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris myocardial infarction; cardiant; antiarteriosclerotic; antianginal; gene therapy; differential gene expression; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                               Predicting, diagnosing or prognosing a cardiovascular disease, angine, ischemia, myocardial infarction or arteriosclerosis by of a polymuclectide in a biological sample comprises detecting hybridization complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1866;
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                            cardiovascular
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                                                                                                                                                                                                                                                                                                        Schmitz
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                            regulated in
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                                                                                                                                                                           GGTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGAC 1799
                                                                                                                                                                                                                 AATCTCCCGCTGCTGCTGCTGCCCCTTACCTTCCCCAGCGTCCCAGTCTCTGCCAG 1512
                                                                                                                                                                                                                                                                                                                                                                                              human; PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic; antirheumatic; dermatological; immunostimulant; immunosuppressive; osteopathic; vasotropic; immune related disease; inflammatory immune response; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; spondyloarthropathy; systemic sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc, capable of stimulating an immune response, useful for treating diseases such as rheumatoid arthritis, psoriasis, and leukopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         idiopathic inflammatory myopathy; Sjogren's syndrome; systemic vasculitis; sarcoldosis; autoimmune haemolytic anaemia; autoimmune disease; immune-mediated skin disease; bullous skin disease; erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
                                                                                                                                          1633 TAGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCC
                                                                                                                                                             GGGCCGAATCCCCTCTCTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGT
                                                                               GGGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCTCATCTCATTCAAACCCCACCC
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                                                                                                                                                                                                                                                         CCGTCTAATATATATATATAGAGATGTGTCTATGGCTG 1850
                                                                                                                                                                                                                                           CCGTCTAATATATAAATATAGAGATGTGTCTATGGCTG 1837
                                                                                                                                                                                                                                                                                                                                                                            Human PRO87334 encoding cDNA SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu TD,
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                                                                                                                                                                                                                                                                                                                 ADO24424 standard; cDNA; 1866 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-2003; 2003WO-US036002
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P-PSDB; ADO24425.
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The present invention describes an isolated human PRO polypeptide (I).

Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a vector (III); (3) a notated PRO nucleic (II) acid encoding (II); (4) producing (II); (5) a chimmeric molecule (V) comprising (III); (4) producing (II); (5) a chimmeric molecule (V) comprising (II) in agoing (II); (4) producing (II); (5) a composition of matter comprising (II), which specifically composition of matter comprising (II), an agoinst of (II), or composition with a carrier; (8) (II), an antagonist of (II), or composition with a carrier; (8) (II), an antagonist of (II), an antagonist of (II), an antagonist of (II), an antagonist of (II), or the antibody (VII); (9) (11), an agoinst of (II), an antagonist of (II), or the antibody (VII); (9) (11), an agoinst of (II), and an antagonist of (II), or the antibody (VII); (9) (11) and antagonist of (II) and (II) and (II) at the same cell type; (I0) identifying a compound that inhibits the expression of a gene encoding (II) identifying a compound that inhibits the expression of a gene encoding (II); and (III) identifying a compound that inhibits to expression of a gene encoding (II); and (III) identifying a compound that inhibits antinament, dermatological, immunostimating the immune response in a mammal. (II) has useful for antinheumatic, dermatological, immunostimulant, immunosuppressive, costeopathic and vasotropic activities. (I) and (VII) are useful for treating mammal having an immune content for the polypeptide. (IVI) is useful for treating mammal having an immune content content sequence of (I) in a sample suspected of containing the presence of (II) in a sample suspected of containing the polypeptide. (IVI) is useful for treating mammal having an immune harmolytic anaemia, autoimmune or immune-immined skind diseases including bullous skind diseases, erythematomatic invented encodes a human PRO protein from the present invente invented invented anuman and protein from the present invented invented and an anamal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                               1633 TAGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCC
                                                 1680 GGGCCGAATCCCCTCTCTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGT
                                                          1693 GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGT
                                                                                                                                                                                                                                             neoplasm; tumor marker; cytostatic; breast tumor; gene therapy;
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                                                                                                                   CCGTCTAATATATATAGAGATGTGTCTATGGCTG 1837
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ADZ10042
ID ADZ10042 standard; DNA; 1866 BP.
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.; 3 The invention relates to a novel method for characterizing the state of a neoplastic disease in a subject comprising determining the pattern of expression levels of at least 6, 8,10,15, 20, 30, 47 or 67 marker genes in a biological sample, comparing the pattern of expression levels with reference patterns of expression levels and characterizing the state of the neoplastic disease in the subject from the outcome of the comparison. The method of the invention demonstrates cytostatic applications and may be useful in characterizing the state of a neoplastic disease in a subject, preferably breast cancer, in gene therapy and for screening for compounds having a curative effect on a neoplastic disease. The current sequence is that of the human breast cancer marker MARKS DNA of the Characterizing the state of a neoplastic disease in a subject by comparing the pattern of determined expression levels of marker genes a biological sample with reference patterns of expression levels. 54; Gaps invention which is differentially expressed in neoplastic tissue. DB 14; Length 1866; Sequence 1866 BP; 380 A; 605 C; 535 G; 346 T; 0 U; 0 Other; 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weducing or reversing tolerance, physical dependence, hyperalgesia,
withdrawal symptoms, or pain sensitization in patients on analgesics for
chronic pain, comprises inhibition of the extracellular signal-regulated
kinase (ERK).
                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of reducing or reversing tolerance, reducing the risk of physical dependence or hyperalgesia, reducing the symptoms of opioid withdrawal or inhibiting pain sensitisation in a patient taking analgesics. The method comprises administering an analgesic and an extracellular signal-regulated kinase (BRK) inhibitor comprised in a formulation to reduce or reverse tolerance, risk of physical dependence, hyperalgesia, symptoms of opioid withdrawal, or inhibiting pain sensitisation in patients taking analgesics for chronic pain or those undergoing surgery. The present sequence represents the coding sequence of human BRKI
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    "Extracellular signal regulated kinase"
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------CAGIGGCCGAGGAGCCTICACCTICGCCAIGGAGCIGGAIGACCIACCIA 1020
                            AGGAGCGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG
                                                                CGCCAGACTGTTAGAAATGGACACTGTGCCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
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                                                      AGGCCCCCTAGCCCAGACAGACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAG
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                                                                                                       Human polynucleotide SEQ ID NO 3685.
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AAI59696 standard; cDNA; 1868
                                                                                     (first entry)
                                                                                                                                                                                    leukaemia; ss
                                                                                     22-OCT-2001
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Homo sapiens

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, concoded polypeptides (AAM38642-AAM42213) with nootropic, concoded polypeptides of cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous of system, such as contains and central nervous system diseases, such as a lateral sed neuropathy and clateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activities such as: Immune system suppression, cutilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolyvic activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form to part of the printed specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids and polypeptides, useful for treating disorders such
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Zhang J,
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Yang Y,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-0059317.
20-JUL-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653450.
14-SEP-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
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Wang J, V
Zhou P, C
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Zhang J, Zhao QA;
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-0059317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00531850.
14-SEP-2000; 2000US-006531450.
14-SEP-2000; 2000US-00653191.
19-CCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
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                                            GTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGCAG
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosas, and Shy-Drager Syndome. Other uses include the utilisation of the activities such as Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form rel nucleic acids and polypeptides, useful for treating disorders central nervous system injuries. Claim 1; SEQ ID NO 113; 10078pp; English WPI; 2001-442253/47 P-PSDB; AAM38754. Novel aB 

Sequence 1869 BP; 378 A; 608 C; 535 G; 348 T; 0 U; 0 Other;

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542 182 243 242 302 362 422 483 482 543 603 602 663 662 123 303 363 423 62 GTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGGCGCTACGGCATGGTCAGC CATCAGACCTACTGCCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCCAT GAGAATGTCATCGGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAGT GTCTACATTGTGCAGGACCTGATGAGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGCAG CTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACATC CACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCACC receacerraagarrrengarrregeceregeceegarrecegarecegarecege ACCGGTTCCTGACGGGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGCTG GTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCAGC TCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCGAA CATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCCAT GTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGCAG CTGAGCAATGACCATATCTGCTACTTCCTCTACAGATCCTGCGGGGCCTCAAGTACATC CACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCACC Gaps Length 1869; 61; 2; Indels DB 4; Score 1679.8; Pred. No. 0; 0; Mismatches Query Match 91.4%; Best Local Similarity 96.6%; Matches 1782; Conservative 543 m 64 63 124 184 183 244 243 304 303 364 363 423 483 544 604 503 664 123 424 484 8 8 Š g

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1492 1612 1672 1142 1512 1632 1732 1022 1143 1272 1321 1332 TGGAGCATGGGCCTGGCCACCTCTCTCTTGCTGAGGCCTCCAGCTTCAGGC-----A 1375 1082 cccacccragirircccraaagaacarrccrragicrccaaggccragcarccrgaggag 1692 964 AAGTCAGACTCCAAAGCCCTTGACCTGGACGGATGTTAACCTTTAACCCCAATAAA 1023 GCCCCCTAG-CCCAGACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAGA 1201 962 782 843 842 903 902 963 722 783 GCCAGACTGTTAGAAAATGGACACTGTGCCAGCCCGGACCTTGGCAGCCCAGGCGGGG creecaerrriegaaregaacegricreecreececaacerearegaagegaagegreea ATGCTCTAACCGGCCCATCTTCCCTGGCAGCACTACCTGGATCAGCTCAACCACTT TTTCCCC ceaaactacctacactcrcccccccaaeaccaaectreeccaaectrreecc AAGTCAGACTCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCCTTTAACCCCAATAAA CGGATCACAGTGGAGGGAGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACG GATGAGCCAGTGGCCGAGGGGCCCTTCACCTTCGCCATGGAGCTGGATGACCTAACG GAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGGAG GCCAGACTGTTAGAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGGCCGGGG GGCCAAGGCCTTCTCCTCCCCACCGCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCC CCAGTTCAATCTCCC---GCTGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCT ccagincaarcrecegerecrecrecrecrecerecerrecerracerreceases CTGGCAGTTCTGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGA GGGTGGGGGGGCGCTGAGGACTCAGGGCCATGCCTGCCCCCCCTCATCTCAAAC GGGTGGGGGCGCTGAGGGACTCAGGGCCATGCCTGCCCCCCCTCATCTCAAAC CCCACCCTAGITICCCTGAAGGAACATICCTTAGICTCAAGGGCTAGCAICCCTGAGGAG CCAGGCCGGGCCGAATCCCCTCCCTGTCAAGCTGTCACTTCGCGTGCCCTCGCTGCTTC AACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTGAG CTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGGCC CGANACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCCAAGCT 1513 904 1023 1083 1143 1245 1262 1273 1322 1333 1376 1393 1436 1453 1493 1553 1573 1613 1633 1673 1693 784 783 844 843 903 963 723 663 유 셤 셤 셤 ò 셤 ઠે 셤 8 셤 ઠે 셤 à 셤 ઠ 요 ઠે g 8 셤 ð 셤 ò 요 δ 8 Š g 8 셤 8 ò 8 Š

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                                                CCCTGACCCGTCTAATATATATAGAGATGTGTCTATGGCTG 1837
                                                            Sequence 1726 BP; 339 A; 562 C; 491 G; 334 T; 0 U; 0 Other;
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/product= "SMAPK3V2 protein"
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                                                                                                                                                                                                   Human SMAPK3V2 variant gene
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1654 BP; 319 A; 536 C; 482 G; 317 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1451; DB 14;
Pred. No. 0;
0; Mismatches 0;
                                                                                                                                                                                              Claim 4; SEQ ID NO 1; 55pp; English
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Best Local Similarity 90.0%;
Matches 1654; Conservative
                                                       WPI; 2005-080923/09
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                                                                              CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCGGACCTTGGCAGCCCAGG
                                                                                                                                                             TCAATCTCCCGCTGCTGCTGCGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT
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                                                          CGCCAGACTGTTAGAAAATGGACACTGTGCCCCAGCCCGGACCTTGGCAGCCCAGGCCGGG
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The invention relates to novel isolated human kinases and phosphatases (KPP) polypeptides. A protein of the invention has cytostatic, anorectic, and immunosuppressive activity, and acts as a KPP-Ahtagonist, or KPP-Agnist. A polymucleotide of the invention may have a use in gene therapy. The polypeptide is useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional KPP e.g., autoimmune disorders, obesity or cancer. The sequences shown in ADH48392-ADH48440 represent KPP proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human kinases and phosphatases (KPP) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional KPP e.g., cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marquis JP, Baughn MR, Tran UK, Hafalia AJA, Kable AE;
Emerling BM, Elliott VS, Lindquist EA, Richardson TW, Khare R
Swarnakar A, Lee SY, Ramkumar J, Chawla NK, Becha SD, Mason I
Hawkins PR, Bulloch SA, Jin P, Bhatia U, Burrill JD, Lee S;
                                                                                                                                                                                                                                                       human; KPP; kinase; phosphatase; enzyme; cytostatic; anorectic; immunosuppressive; KPP-Antagonist; KPP-Agonist; gene therapy; autoimmune disorder; obesity; cancer; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 187;
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                                 1618 CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.2%; Score 1437; DB 12;
ilarity 89.8%; Pred. No. 0;
Conservative 0; Mismatches 0;
               1801 CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
25. .1032
/*tag= a
                                                                                                                                                                                                                       Human KPP encoding DNA SEQ ID NO:71
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Matches 1654; Conserv
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	Oy 1261 CGCCAGACTGTTAGAAATGGACACTGTGCCCAGCCCGGACCTTGGCCAGGCCCGGG 1320 	1321	1381 AGGCCTTCTCCCCACCGCCTTCCCCACGGGGCCTCGGGAGCTCAGGGGCCCCAGGT  1211 AGGCCTTCTCCTCCCCACCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGGGGCCCCAGT  1211 AGGCCTTCTCCTCCACCGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT  1211 AGGCCTTCTCCTCCACCAGGCCCTCCCCACGGGGCCTCGGGAGCTCAGGTGGCCCCAGT	1441 TCAATCTCCGGTGCTGCTGCTGCCCTTACCTTCCCCAGGGTCCAGGTCTGGGTCCTGGTTACCTTCCCCAGGTCCCAGGTCTCTGGTTACCTTCCCCAGGTCCCCAGGTCTCTGGTTACTTCCCCAGGTCCCCAGGTCTCTGGTTACTTCCCCAGGTCTCTGGTTACTTCCCCAGGTCTCTGGTTACTTCCCCAGGTCTCTGGTTACTTCCCCAGGTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCTCTGGTTACTTCCTTC	1497 CAGTICTGGAATGGAAGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAAGGGTGGAGGGTTCTGGATGGA	1557 @GGGGGCCTGACTAGGGACTCAGGGCCATGCCCCCTCATCTCATTCAAACCCCATGATTCAAACCCCATGATTCAAACCCCATGATTCAAACCCCATGATTCAAACCCCCATGCCTGCC		GCCGGGCCGAATCCCCTCCTGTCAAAGCTGTCACTTCGCGTGCCTCGCTGCTTCTGTG	TGTGGTGAGCAGAAGTGGAGCTGGGGGGCGTGGAGAGCCCGG 	Qy         1797         DACCCGTCTAATATATAAATATAGAGATGTGTTATGGCTG         1837	RESULT 15 ADH59631 ID ADH59631 standard; DNA; 1140 BP.	AC ADHS9631; XX YS OF UND JOAN (Figure parties)	encoding sequen	XX	sapiens.	FT CDS 11140 FT /*tag= a FT /product= "Erk1"	D 27-MAR-2003.	XX PF 18-SEP-2002; 2002WO-EP010489.
CCGAGGGGTCGGCCCGGGGGTCCCGGGGGAGATGGTGAAGGGGCAGCCGTTCG	ACGTGGGCCCGCGCTACACGCAGTTGCAGTACATCGGCGAGGGCGCGTACGGCAA GGTCGGCCTATGACACGCGCAAGACTCGCGTGGCTGGCCATCAAGAAGATCAGCCC		301 ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGGGTCCACCCTGGAAGCCATGAGAG 360 	361 ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC 420 		481 TCCACTCCGCCAACGTGCTCCCAGAGATCTAAAGCCCTCCAACCTGCTCAACACCA 540	CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCGGATTGCCGATCCTGAGCATGACC	ACACCGGCTTCCTGACGGGTATGTGGCTACGGGCTGGTACGGGCCCCAGAGATCATGCTACGGGCTGGTACGGGCTGGTACGGGCTGGTACGGGCTGGTACGGGCTGGTACGGGCTGGTACGGGCCCCGGGAGATCATGCTACGGCTGGTACGGTGGTACGGCCCCAGAGATCATGGCTACGGCTGGTACGCCCAGGAGATCATGGCTACGGCTGGTACGCCAGGAGATCATGGCTACGGCTGGTACGGCTGGTACGGCCAGGAGATCATGGCTACGGCTAGGTACGAGCTACGGCTAGGAGATCATGGCTACAGGCTACGGCTAGGAGATCATGGCTACAGGCTAGGAGATCATGGCTAGAGATACATGGCTAGAGATACATGGCTAGAGATACATGGCTAGAGATACATGGCTAGAGATACATGGCTAGAGATACATGGAGAGATCAATGGAGAGATCAATGGAGAGATCAATGGAGAGATCAATGGAGAGATCAATGGAGAATGAAT	TGAACTICCAAGGGCTATACCAAGTICCATCGACATITGGTICTGTGGGCTGCATTCTGGCTG	AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACAAGTGCTCTAACCACAAAGCTCTAACCTGGATCAGCTCAACCACAAGTCTCTCTC	781 TTCTGGGCATCCTGGGCTCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG 840        794 TTCTG798	CCCGAAACTACCTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCC	799			1021 CGGATGAGCCAGTGGCCGAGGAGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCT	1081   AGGAGCGGCTGAAGGAGCTCATCCAGGAGACAGCACGCTTCCAGCCCGGAGTGCTGG	

Brinkmann K;

Funk M, Reuner B,

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Leclair

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The present invention relates to identifying and obtaining a compound useful in the prevention or treatment of cardiac diseases, comprising compartication of the activity of Raf-1, MEXI/2 and/or Erki/2 depending on the compound. The method is useful for identifying and/or obtaining compounds that may be used in the prevention or treatment of cardiac diseases, particularly congestive heart failure. The compound or protein is also used for the preparation of a pharmaceutical composition for prevention or treatment of a disease related to hypertrophy or impaired or increased activation of telethonin (T-Cap), kagr;-actinin, MEC, actin, the protein or antibody which specifically recognizes the activated/phosphorylated form of the above polypeptide, is used for the protein or actibody which specifically recognizes the activation of a composition for diagnosing a disease or a predisposition for diagnosing a disease or a predisposition for cativation of Raf-1, MEXI/2 and/or Erki/2. The present sequence
                                                                                                                                                                                                                                            Identifying and/or obtaining a compound useful for preventing or treating cardiac diseases, particularly congestive heart failure, comprises quantification of the activity of Raf-1, MEK1/2 and/or Brk1/2 depending
                                                                                                                                                                                                                                                                                                                                                        Claim 33; SEQ ID NO 7; 41pp; English
                 19-SEP-2001; 2001US-0323566P. 24-SEP-2001; 2001US-0324625P.
                                                                                                                       Roenicke V,
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                                                                                  (MEDI-) MEDIGENE AG
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                                                                                                                                                 Henkel
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Seguence 1140 BP; 247 A; 357 C; 324 G; 212 T; 0 U; 0 Other;

Gaps DB 10; Length 1140; ; 0 1; Indels Score 1138.4; DB 10 Pred. No. 2.2e-247; 0; Mismatches 1; 62.0%; 99.9%; Best Local Similarity 99.9 Matches 1139, Conservative Query Match

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1031 1020 1091 1080 1151 1140 600 999 780 840 900 960 551 611 671 731 720 791 851 911 971 GTGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACGACGGATGAGCC AAGGAGCTCATCCTCCAGGAGACAGCACGTTCCAGCCCGGAGTGCTGGAGGCCCCCTAG 481 AACGIGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCAGCAACACCACCTGCGGACCTT CTGACGGAGTATGTGGCTACGCGCTACCGGGCCCCCAGAGATCATGCTGAACTCCAAG CTGACGGAGTATGTGGCTACGGGCTGGTACCGGGCCCCAGAGATCATGCTGAACTCCAAG GCTATACCAAGTCCATCGACTGGTCTGTGTGTTTTTGGCTGAGGTCTCT AACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACATTCTGGGCATC CTACAGTCTCTGCCCTCCAAGACCAAGGTGGCTTTGGGCCAAGCTTTTCCCCAAGTCAGAC TCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTTAACCCCCAATAAACGGATCACA GTGGAGGAAGCGCTCACCCTACCTGGAGCAGTACTATGACCCGACGGATGAGCCA AACGIGCICCACCGAGAICIBAAGCCCICCAACCIGCICAICAACACCACCIGCGACCII GGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTGAGATGCTCTCT CTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGGCCCGAAACTAC 1032 1021 1092 541 912 901 196 492 552 612 601 672 661 732 721 792 781 852 841 972 셤 à g Š 셤 ò 셤 Š 셤 ઠે g ઠે q ò g ઠે g 8 В ò

7, 2006, 12:49:02 completed: February ne : 1133.96 secs time Search Job time

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Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
               ALSS9377 ALSS9781539 ACST6647 ALSS9763 ALSS9764 BX444546 BX444546 BX44546 BX44546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR620058 1775 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DA001YE10 of Neuroblastoma of Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini; Hominidae, Homo.

1 (base 1 to 1775)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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93.2%; Score 1712.4;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches
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CR620058.1 GI:50500865
HTC; CNSLT_CDNA.
HOMO sapiens (human)
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AUTHORS
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Best Local Similarity 97.1%; Pred. No. 0;
Matches 1761; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirced.
                                                              CR606522 1764 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DD004YA12 of Neuroblastoma Cot
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                 Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 1764;
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1 (bases 1 to 1764)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished
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/organism="Homo sapiens"
/mol type="mcNA"
/db_xref="taxon:9606"
/clone="CSDDDO04YAL2"
/tissue_type="Neuroblastoma CK/plasmid="pcMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%; Score 1694.4;
.larity 97.1%; Pred. No. 0;
Conservative 0; Mismatches
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HTC; CNSLT_cDNA.
Homo sapiens (human)
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1397   TCAATCTCCCGCTGCTGCTGCCCCTTACCTTCCCCAGCGTCCTGGCAGT   1456	RESULT 4  CR595737  CR595737  CR595737  CR595737  CR595737  ACCESSION  CR595737  CR595737  ACCESSION  CR595737  CR59573  CR595737  CR595737  CR59573  CR59573  CR59667  CR5070  CR5070		Similarity 97.1%; Pred. No. 0; 0; Conservative 0; Mismatches 1; I CGGCGGCGGCGCTCAGGGGGGGGGGGGGGGGGGGCCCCGTA

TITLE Direct Submission  JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1	Query Match         91.5%; Score 1681.4; DB 4; Length 1751;           Best Local Similarity 97.1%; Pred. No. 0;         1, indels 51; Gaps           Matches 1743; Conservative 0; Mismatches 1; Indels 51; Gaps         1 Indels 51; Gaps           1 GAGGAGTGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGG	121 ACGTGGCCCGGGCTACAACGCAGTTGCAGTGGGGGGGGGCGTGCGGGAGGGCGCTACACGGCATGGTCA  128 ACGTGGGCCTACACGCGCAGTTGCAGTTACATCGGCGAGGGCGCTACGGCATGGTCA  128 ACGTGGGCCTACACGCGCAAGACTCGGGTGGCCATCAAGAAGATCAGGCCTTCG  181 GCTCGGCCTATGACCACGTGGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG  241 AACATCAGACCTACTGCCAGCGCACGCTCCGGGGAATCCTCGCTGCGCCTTCG  242 AACATCAGACCTACTGCCAGCGCACGCTCCGGGAATCCTGCTGCGCTTCGCC  243 AACATCAGACCTACTGCCAGCGCACGCTCCGGGAATCCTGCTGCGCTTCCGCC  301 ATGAGAATGTCATCGGCACGCTCCGGGAATCCTGCTGCTGCTTCCGCC  10	Db 308 ATGAGAATGTCATCGGCATCCGGGGCGTCCACCCTGGAAGCCATGAGAG 367  Qy 361 ATGTCTACATTGTGCAGGACCTGATGGACTGACAGTTGTGTGAAAAGCCAGC 420  Db 368 ATGTCTACATTGTGCAGGACCTGATGGACTGACCTGTACAGTTGCTGAAAAGCCAGC 427  Qy 421 AGCTGAGCAATGCCATATCTGCTACTGTACCAGATCTGTGAAAAGCCAGC 427  Qy 428 AGCTGAGCAATGACCATATCTGCTTACCAGATCCTGCGGGGCCTCAAGTACA 487  Qy 489 TCCACTCGCCAACAGTGCTCCTCTACCAGATCTGCGGGGCCTCAAGTACA 487  Qy 489 TCCACTCGGCAACTGCTCCACCAGATCTTACCAGATCTGCGGGGCCTCAACACCA 540  Qy 541 CCTGCGCAACAGTGCTCCACCAGAATCTTACAGATCTACCAACACCACACCACCAACACACAC	Qy         601 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC 660           bb         608 ACACCGGCTTCCTGACGAGTATGTGGCTACGGGCTCGTGGTGCTCCTGGGGCCCCCAGAGATCATGC 667           Qy         661 TGAACTCCAAGGGCTATACCAAGTCCATCGACTCTGTGGGCTGCATTCTGGCTG 720           bb         668 TGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCTG 720           Qy         721 AGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACGGGTTCAGGCTCAACCACA 780
1081 AGCTCATCTTCCAGGAGACAGCACGCCGGAGGTGCTGGAGGCCCCTTAGCCC 1140   1156 GACAGACATCTTCCAGGACCTGGAACAGAACTGGCAAAGAGGCCAAGAGTCAT 1215   1		1510 1636 1570 1630 1756 1756	Qy 1816 TA 1817  Db 1750 TA 1751  RESULT 5  CR597147  LOCUS  CR597147  LOCUS  CR597147  CR597147	Hominidae, Homo.  Hominidae, Homo.  AUTHORS 1 (bases 1 to 1751)  AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  TITLE Pull-length cDNA libraries and normalization  JOURNAL Unpublished  Contact: Feng Liang Email: fliangelifetech.com URL:  http://fulllength.invitrogen.com/ InVitroGen Corporation 1600  REFERENCE 2 (bases 1 to 1751)  AUTHORS Genoscope.

CR603463 1854 bp mRNA 1 fill-length cDNA clone CS0DN005XA14 of Add	(human). CR603463 CR603463. GI:50484270 HTC: CNSIT CDNA.	Homo sapier Homo sapier Homo sapier Eukaryota;	Hominidae, Homo.  1 (bases 1 to 1854) Li, W.B., Gruber, C., Full-length cDNA lib	Unpublished Contact : Feng Liang Email : fliang@lifete http://fulllength.invitrogen.com/ InVitro Faraday Avenue	2 (bases to 1854) Genoscope. Given Submission Submission Submitted (20-mm-2004) Genoscope	BP 191 91006 EVRY cedex - FRANCE (B-mail - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a Not1-ol:	into the Not I and Book V sites of the powar normalized. Library was constructed by division of Invitrogen.		/clone="CSODNO05YA14" /tissue_type="Adult_brain" /plasmid="pcMVSPORT_6"	Ouery Match  Query Match  Query Score 1673.4; DB 4  Query Match  91.1%; Score 1673.4; DB 4  96.2%; Pred. No. 0;  Marchen 1762: Conservative 0; Mismatches 1;	ABT	61 CCGAGGGGGTCGGCCCGGGGGTCCCGGGGGAGGTGGAGA 13-5 CCGAGGGGGTCGCCCGGGGGAGGTGGAGA	121 ACTIGGGCCCGCCTACACCCAGTTGCAGTACATCGCCG 125 ACGTGGCCCGCCTACACGCAGTTGCAGTACATCGCCG 195 ACGTGGCCCGCCTACACGCAGTTGCAGTACATCGGCG	181 GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCAAGACTCGCGTGGCCAAGACACGTGCGCAAGACTCGCGCAAGACTGCGCAAGACTGCGCAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCGAAGACTGCAAGACTGCGAAGACTGCAAGACTGCAAGACTGCAAGACTACAAGACTGCAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAGACTACAAAAAAAA		301 ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGGGT 	361 ATGTCTACATTGTGCAGGACCTGATGGAGACTGACTGT
CR603463 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE	REFERENCE AUTHORS TITLE	JOURNAL	REFERENCE AUTHORS TITLE	COMMENT	odamkaa	BOULCE	NICTOO	Query M Best Lo	₩ ₩	ે કે કે	8 & 8	\ & &	1 & A	95 63	ζ <b>ο</b>
11	781 TTCTGGGCATCCTGGGCTCCCCATCCCAGAGGACCTGAATTGTATCATCAACATGAAGG 840 	841 CCCGAAACTACCTACAGTCTCTGCCCTCCAAGGTGGCTTGGGCCAAGCTTTTCC 900	901 CCAAGTCAGACTCCAAAGCCCTTGACCTGGTGGCGGGTGTTAACCTTTAACCCCAATA 960 	961 AACGGATCACAGTGGAAGCGCTGGCTCCCTACCTGGAGCAGTACTATGACCCGA 1020 	1021 CGGATGAGCCGTGGGGCCCTTCACCTTCGCCATGGAGCTGGATGACCTACCT	1081 AGGAGCGGCTGAAGGACTCATCTTCCAGGACAGCACGCTTCCAGCCCGGAGTGCTGG 1140	1141 AGGCCCCTAGCCCAGACACATCTCTGCACCTCGGAGCCTCGAACACAGAACTCGCAAAG 1200 	1201 AGGCAAGAGTCACTGAGGCCTCTGTCACCCAGGACTGCCTCTGCTGCCCTCTCC 1260	1261 CGCCAGACTGTTAGAAAATGGACACTGTGCCCAGCCCCGGACCTTGGCAGCCCAGGCCGGG 1320 	1321 GTGGAGCATGGCCACCTCTCTCTTGCTGAGGCCTCCAGCTTCAGGCAGG	1381 AGGCCTCCCCCCCCCCCCCCCCCCCCCCCCGGGGCCTCGGGAGCTCAGGTGGCCCCAGT 1440	1441 TCAATCTCCCGCTGCTGCTGCTGCCCCTTACCTTCCCCAGCGTCCCCAGTCTCTCGCAGT 1500	1501 TCTGGAATGGAAGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGTGGAGGTGGGG 1560 	1561 GGCGCTGAGTAGGGACTCAGGGCCATGCCCCCTCATCTCATTCAAACCCCACCT 1620 	TCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG 	GGCCGAATCCCTTCCTGTCAAAGCTGTCACTTCGCTGCCCTCGCTGCTTCTGTGTGTTGT 	1741 GTGAGCAGAAGTGGGGGGGGGGGGGGGGCCCGGCCCCTGCCACTCCC 1795 
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oligo (dT) primer. Five prime gested with Not I and cloned pCMVSPORT 6 vector. Library by Life Technologies, a ñ GATGGTGAAGGGCAGCCGTTCG 120 CATCAAGAAGATCAGCCCCTTGG 240 CCAGATCTGCTGCGCTTCCGCC 300 linear HTC 21-JUL-2004 Adult brain of Homo sapiens CGAGGGGGGTACGGCATGGTCA 180 421 AGCTGAGCAATGACCATATCTGCTACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACA 480 re National de Sequencage : seqref@genoscope.cns.fr GGGGGGGGGGGCCCCGTAGAA 60 Vertebrata; Buteleostomi; ; Indels 68; Gaps tech.com URL : coGen Corporation 1600 4; Length 1854; aB, D.

1524   TCCCAGTCTCTGGCAGTGCAATGGAAGGGTTCTGGCTGCCCCAACCTGAAGGGC   1583   1544   AGAGGTGGAGGGGGGGGGGGAGGAGGATCTGGCCTGCCCCCTCATCT   1603   1584   AGAGGTGGAGGGGGGGGGGGAGAGACTCAGGGCCATGCCTGCC	Z	Σ	Faraday Avenue   Faraday Avenue	rce	10-normalized"
8 8 8 8 8 8 8 8 8 8	RESULT 7 CR621977 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	OKGANISM REFERENCE AUTHORS TITLE JOURNAL REMARK	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	ORIGIN Query Me Best Loc Matches Qy
495 AGCTGAGCAATGCCATATCTGCTACCAGATCCTGCGGGGCCTCAAGTACA 554  481 TCCACTCGCCCAACGTGCTACTTCTTCTCTACCAGATCCTGCGGGGCCTCAAGTACA 554  481 TCCACTCGCCCAACGTGCTCCACCGGATCTAAAGCCCTCCAACCTCATCAACACCA 540			1064 GCTGGATGACCTACCTAAGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTT 1123	1184 GAACAGAACTGGCAAAAGGCCACTGAGGCCTCTGTCACCCAGGACTGCCT 1243	1344 TGGCGGGGGGGGGGGGGCTGGCACCTCTCTCTTGCTGGGGCCTC 1403  1364 CAGCTTCAGGCGGGGGGGGCTGGCCTCCCCCCCCCCCCC

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	CR621688  CR621688  (111)-length CDNA clone CS0D1044FF16 of Placenta Cot 25-normalized of Homo sapiens (human). CR621688  CR621688  CR621688.  CR621688.  CR621688.  GR521688.  GR521688.
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                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/clone="CSODI044YF16"
/tissue_type="Placenta Cot 2
/plasmid="pcMvSPORT_6"
                                                                                                                                         Score 1644.4;
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DRGANISM Homo sapiens  ENKAYOFAE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;  Hominidae; Homo.  REPERENCE  I (bases 1 to 1678)  AUTHORS  II, W.B., Gruber, C., Jessee, J. and Polayes, D.  TITLE  TITLE  Unpublished  Contact: Feng Liang Email: Eliang@lifetech.com URL:  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  REFERENCE  REMARK  AUTHORS  PARAGA Avenue  REMARK  AUTHORS  AUTHORS  Infect Submission  JOURNAL  Submisted (20-JUJ-2004) Genoscope - Centre National de Sequencage:  JOURNAL  Submisted (20-JUJ-2004) Genoscope - Centre National de Sequencage:  BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  - Web: www.genoscope.cns.fr)  1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned	into the Not I and ECOR V sites of the pCMVSPORT 6 Vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  FEATURES  Location/Qualifiers  1. 1678  / Organism="Homo sapiens" // Mol_type="mRNA" // Alba="CSOBCO16YPQE" // Clone="CSOBCO16YPQE" // Clone="CSOBCO16YPQE" // Lissue type="Neuroblastoma Cot 25-normalized" // Lissue type="Neu		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-70L-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1.1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:960"
/clone="CSODL009YH16"
/tissue type="B cells (Ramos cell line) Cot 25-normalized"
/plasmid="pcMvSPORT_6"
    HTC 21-JUL-2004
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1 (bases 1 to 1/18)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                                                                                                           CRS96064 1718 bp mRNA linear HTC 21-JUL-2 full-length cDNA clone CSODL009YH16 of B cells (Ramos cell line) Cot 25-normalized of Homo sapiens (human).
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http://fulllength.invitrogen.com/ inVitroGen Corporation 1600
Faraday Avenue
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                                    GGAGCTGGGGGGGGTGGAGAGCCCGGCCCCTGCCACCTCCCTGACCC
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93.8%; Pred. No. 0;
iive 0; Mismatches
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Homo sapiens
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                                                                     GTGGCCATCAAGAAGATCAGCCCCTTCGAACATCAGACCTACTGCCAGCGCACGCTCCGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCCCCTCATTCAAACCCCACCCT
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  AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGCCTCGGGACCTCAGGTGGCCCCAGT
                                 TCTGGAATGGAAGGGTTCTGGCTGCCCCAACCTGCTGAAGGGCAGAGGGTGGAGGGTGGGG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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1 (bases 1 to 1612)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length CDNA libraries and normalization
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/tissue type="Neuroblastoma
/plasmid="pcMVSPORT_6"
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/mol_type="mRNA"
/db xref="taxon:9606"
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HTC; CNSLT_cDNA.
Homo sapiens (human)
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FEATURES  Location/Qualifiers  11130  /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:5606" /clone="CSODD008YK04" /tissue type="NEUROBLASTOMA COT 50-NORMALIZED" /clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="list strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	Query Match         56.3%;         Score 1034.2;         DB 1;         Length 1130;           Best Local Similarity         97.1%;         Pred. No. 5.2e-224;         Antches 1054;         Conservative         8;         Mismatches 21;         Indels 2;         Gaps 1;           Qy         15         GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	75 C 64 C 135 T C 124 T T T C 124 T T T T T T T T T T T T T T T T T T T	Oy 195 CACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCGAACATCAGACCTAC 254	Qy         315         GGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGATGTCTACATTGTG         374           Db         304         GGCATCCGAGACATTCTGCGGGCGTCCACCCTGGAAGCCATGAGAGATGTCTACATTGTG         363           Qy         375         CAGGACCTGAACGACTGAACCTGTACAACTGCTGAAAAGCCAAGCAATGAATG		Db 544 ATTGTGATTTGGGCCTGGTACCGGTCTCTGGGCTTCCTG 603  Qy 615 ACGGAGTATGTGGCTACGCGCTGGTACCCGGCTTCCTG 603  Qy 615 ACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGCTGAACTCCAAGGGC 674  Db 604 ACGGAGTATGTGGCTACGGGTCTGTGGGCCCCCAGAGATCATGCTGAACTCCAAGGGC 663  Qy 675 TATACCAAGTCCATCGGTCTGTGGGCTGCATTCTGGCTGAGTGCTCTTAC 734  Qy 735 CGGCCATCTTCCCTGGTCTGTGGGCTGCATCTGGCTGAGATGCTCTTAC 723  Qy 735 CGGCCATCTTCCCTGGAGTCTACCTGGATCAGCTCAACCAATTCTGGGCATCTGGTTTTTGGCTATCTTGGGCATCTTTTTTTT
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                                                              TCGACATCTGGTCTGTGGGCTGCATTCTGGCTGAGATGCTCTCTAACCGGCCCATCTTCC
                                                                              CTGGCAAGCACTACCTGGATCAGCTCAACCACATTCTGGGCATCCTGGGC-TCCCCATCC
                                                                                                                                         CTTGMAAGCACTACCTGGATCAGCTCAACCACATTCTGGGCATCCTGGGCYTCCCATCC
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Is (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12794147.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

Z rue Gaston Cramieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                            GAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACGGATGAGCCAGTG 1034
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSGDD08YK04"
/tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED
/olone lit and clone with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                      CAGTCTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCCCCAAGTCAGACTCC
                                                                               GCCTGGCCCGGATTGCCGATCCTGAGCATGACCACACGGCTTCCTGACGGAGTATGTGG
                                                               AAAGCCCTTGACCTGGACCGGATGTTAACCTTTAACCCCAATAAACGGATCACAGTG
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      CAGTCTCTGCCCTCCAAGACCAAGGTGGCTT
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BX445445 Homo sapiens ADULT BRAIN Homo sapiens CDNA clone CSODN005YA14 3-PRIME, mRNA sequence.
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             247 AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC 306
                                                                 ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGGCCTCCACCCTGGAAGCCATGAGAG 360
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                      TTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAGG
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                                                                                                                                                                 ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAAGCCAGC
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                                                                                                                                          ATGICTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC
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                                                                                                                                                                                                                                                                                       TCCACTCCGCCAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGCTCATCAACACCA
                                                                                                                                                                                                                                                                                                                                                                CCTGCGACCTTAAGATTTGTGATTTCGGCCTGGCCCCGGATTGCCGATCCTGAGCATGACC
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1 (bases 1 to 1108)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30770386.

Contact: Genoscope

Genoscope - Centre National de Sequencage
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BX445445.2 GI:46958964
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
nd enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCNVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8342.f
                                                                                                                                                                 AL530980 1016 bp mRNA linear EST 24-MAR-2004
AL530980 Homo sapiens NECROBLASTOMA COT 50-NORWALIZED Homo sapiens
CDNA clone CSODD003YH16 5-PRIME, mRNA sequence.
GTCACTTCGCGTGCCCTCGCTGCTTCTGTGTGTGTGAGCAGAAGT-GGAGCTGGGGGGC 1765
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/mol_type="mRNA"

/mol_type="mRNA"
/mol_type="mRNA"

/db xref="taxon:9606"
/clone="CSODDO03YH16"
/tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="lit strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 1016)

1 (bases 1 to 1016)

1 (bases 2 to 1016)

1 (bases 2 to 1016)

Full-length CDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:31068813.
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Pred. No. 3.3e-207;
4; Mismatches 2;
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SOURCE
ORGANISM
                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                        ACCESSION
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AUTHORS
TITLE
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSFORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invirogen.
This sequence belongs to sequence cluster 8342.f
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?e=CSIAN002ZA08NP1&c=8342.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACGGATGAGCCAG 1032
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/dev_erage="adult"
/clone lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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                                                                                                                                                                                                                   /organism="Homo sapiens"
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|db_xref="taxon:9606"
|clone="CSODNOG5XA14"
|tissue_type="ADULT BRAIN"
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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US-08-463-862-1

US-08-461-985-1

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US-08-932-012C-1

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US-09-742-2

US-09-742-2

US-09-112-289-2

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US-09-412-289-1
US-09-412-289-1
Sequence 1, Application US/09412289
Patent No. 6271210
GENERAL INFORMATION:
APPLICANT: Sivaraman, Vimala S.
APPLICANT: Manbon, Craig C.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED TITLE OF INVENTION: PROTEIN KINASES AS THERAPY FOR CANCER
FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)
CURRENT APPLICATION NUMBER: US/09/412,289
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Best Local Similarity 97.0%;
Matches 1783; Conservative
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US-09-412-289-1
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Pred. No. 0;
0; Mismatches
CURRENT FILING DATE: 1999-10-05
EARLIER APPLICATION NUMBER: 08/909,742
EARLIER PILING DATE: 1997-08-12
EARLIER APPLICATION NUMBER: 08/831,994
EARLIER PILING DATE: 1997-04-01
EARLIER PILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.0%;
Best Local Similarity 97.0%;
Matches 1783; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy 
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; Patent No. 5595904
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
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STRANDEDNESS: single
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CITY: New York
STATE: New York
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US-08-176-620A-1
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                                                                                                                GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.0%; Score 1138.4; DB 3; Length 1896; 99.9%; Pred. No. 8.5e-226; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EGFP-Erkl fusion construct
              RESULT 3
US-09-417-197-38
; Sequence 38, Application US/09417197
; Patent No. 6518021
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.9
Matches 1139; Conservative
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US-09-417-197-38
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LOCATION: (1)
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MAP2 PROTEIN KINASES
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TITLE OF INVENTION: A FAMILY OF MAP2 PRC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08463862; Patent No. 5776751; GENERAL INFORMATION:
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                                                                                              55.8%; Score 1025; DB 2;
.larity 78.1%; Pred. No. 2.1e-202;
Conservative 0; Mismatches 310;
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                    MOLECULE TYPE:
                                           , NAME/KEY:
, LOCATION:
US-08-176-620A-1
                                                                                                             Best Local Sim:
Matches 1391;
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                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentln Belease #1.0, Version #1.25
CORRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,862
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 6526-049
TELEFPANCE/POCKET NUMBER: 6526-049
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Pred. No. 2.1e-202;
0; Mismatches 310;
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 78.1%;
Matches 1391; Conservative
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US-08-463-862-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
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US-08-458-887-1
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                                   13.78 CCAAGGCCTTCTCCCCCACCCGCCCTCCCCACGGGGCCTCGGGGAGCTCAGGTGGCCCC
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APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Lealle
NAGISTRATION NUMBER: 18,922
REFERENCE/DOCKET NUMBER: 6526-049
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Patent No. 5914261
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Boulton et al.
ENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
ENTION: KINABES
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          TITLE OF INVENTION: ANTIBODIES DIRECTED TOWAR TITLE OF INVENTION: KIRASES
FILE REFERENCE: REG 430-A-1
CURRENT APPLICATION NUMBER: US/08/932,787B
CURRENT FILING DATE: 1997-09-18
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1994-01-07
PRIOR PILING DATE: 1994-01-07
PRIOR APPLICATION NUMBER: 08/178,488
PRIOR FILING DATE: 1994-01-07
PRIOR FILING DATE: 1994-01-07
PRIOR FILING DATE: 1994-06-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FREESEQ FOR MINDOWS Version 3.0
SEQ ID NO 1
LENGTH: 1747
TYPE: DNA
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OTHER INFORMATION: ERK1 CDNA
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Best Local Similarity 78.1
Matches 1391; Conservative
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NAME/KEY: CDS
LOCATION: (1).
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Sequence 1, Application US/08932787B Patent No. 6277963 GENERAL INFORMATION:

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55.8%; Score 1025; DB 3; Length 1
Best Local Similarity 78.1%; Pred. No. 2.1e-202;
Matches 1391; Conservative 0; Mismatches 310; Indels
1797 GACCC---GICTAATATATAAATATAGAGATGTGTCTATGG 1834
                 APPLICANT: BOULTON et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
FILE REFERENCE: REG 430-Y-1
CURRENT APPLICATION UNMERS: US/08/932,012C
CURRENT FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 08/462,874
PRIOR FILING DATE: 1995-06-05
FRIOR PELING DATE: 1995-06-05
FRIOR PELING DATE: 1994-01-07
FRIOR PELING DATE: 1994-01-07
FRIOR FILING DATE: 1991-05-06-05
FRIOR FILING DATE: 1991-05-06-01
FRIOR FILING DATE: 1990-06-01
FRIOR FILING DATE: 1990-06-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FRAELSEQ for Windows Version 3.0
                                                                                                                         Sequence 1, Application US/08932012C
Patent No. 6297035
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COTHER INFORMATION: ERK1 CDNA
US-08-932-012C-1
                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1747
TYPE: DNA
ORGANISM: RAT
FEATURE:
NAME/KEY: CDS
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Sequence 1, Application US/0888818C

Sequence 1, Application US/0888818C

Sequence 1, Application US/0888818C

GENERAL INFORMATION:

TITLE REPERENCE: REG 430-V-1

CURRENT FILING DATE: 1997-07-07

PRIOR APPLICATION NUMBER: US/08/888,818C

CURRENT FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/478,985

PRIOR APPLICATION NUMBER: 08/178,488

PRIOR APPLICATION NUMBER: 07/701,544

PRIOR APPLICATION NUMBER: 07/701,544

PRIOR APPLICATION NUMBER: 07/532,004

PRIOR PILING DATE: 1990-06-01

PRIOR PILING DATE: 1990-06-01

SOFTWARE: FSC 1D NOS: 21

SEQ 1D NO 1

LENGTH 1747
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Best Local Similarity 78.1%; Pred. No. 2.1e-202;
Matches 1391; Conservative 0; Mismatches 310;
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OTHER INFORMATION: BRK1 CDNA
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Sequence 56, Application US/09417197

Patent No. 6518021
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: On A Cellular Response
TITLE OF INVENTION: DATE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 56
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Pred. No. 1.1e-188;
0; Mismatches 114;
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90.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.0
Matches 1027; Conservative
                                                     GAGGCACTGAGT
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; NAME/KEY: CDS
; LOCATION: (1)..(1872)
US-09-417-197-56
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                                                                                                                               Length 1701;
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                                                                                                                               Score 651.4; DB 3;
Pred. No. 2.8e-125;
0; Mismatches 282;
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4048
LENGTH: 1701
                                                                                                                                35.5%;
                                                                                                                              Query Match
Best Local Similarity 74.4
Matches 819; Conservative
                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4048
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Batent No. 6812339

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES 7

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES 7

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PPLICATION NUMBER: 60/21,755

PRIOR PPLICATION NUMBER: 60/21,768

PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                                                 1190 riccacardesarriccardacricccraaccaaaaccrcaaacaacraarrirrcaacac 1249
     1010 AATAAGGTGCCATGGAACAGGCTGTTCCCAAATGCTGACTCCAAAGCTCTGGACTTATTG 1069
                                                                                                                                                          CCCTACCTGGAGCAGTACTATGACCCGACGGATGAGCCAGTGGCCGAGGAGCCCTTCACC 1052
                                                        GACCGGATGTTAACCCTTTAACCCCAATAAACGGATCACAGTGGAGGAAGCGCTGGCTCAC
                                                                                                      GACAAAATGTTGACATTCAACCCACACAAGAGGATTGAAGTAGAACAGGCTCTGGCCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED PROTEIN KINASES AS THERAPY FOR BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.2%; Score 646.6; DB 3; 73.2%; Pred. No. 2.8e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,742
FILING DATE: August 12, 1997
CLASSIPICATION NUMBER: US/08/31,994
PRIOR APPLICATION NUMBER: 08/831,994
FILING DATE: April 1, 1997
PRIOR APPLICATION NUMBER: 08/827,520
FILING DATE: MARCH 28, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Adams, Lindbay S.
NAME: Adams, Lindbay S.
VALISHER ADAMS SA 4225
COMPUTER ADAMS SA 4225 CIP INTORNATION SA 4225
COMPUTER ADAMS SA 4225
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ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                       ACAGCACGCTTCCAGCCCGGA 1133
                                                                                                                                                                                                                                                                                                                                                                                                                        1250 ACTGCTAGATTCCAGCCAGGA 1270
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Patent No. 6007991
GENERAL INFORMATION:
APPLICANT: Vimala S. Sivaraman
APPLICANT: Haten-Yu Wang
APPLICANT: Craig C. Malbon
ITILE OF INVENTION: ANTISENSE OLIC
TITLE OF INVENTION: ARTIVATED PROT
ITILE OF INVENTION: BREAST CANCER
WUMBER OF SEQUENCES: 4
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REGISTRATION NUMBER: 36,425
REPRENCE/DOCKET NUMBER: 178-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEPAX: (516) 822-3552
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1611 nucleotides
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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Best Local Similarity
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STATE: New YOU
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HYPOTHETICAL:
ANTI-SENSE:
US-08-909-742-2
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US-08-909-742-2
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746 TCCATTCAGCTAACGTTCTGCACCGTGACCTCAAGCCTTCCAACCTGCTGCTCCAACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BOOT PETFOR PC-DOS/MS-DOS
SOFTWARE: WOOT PETFOCT 6.1 for Wind
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEREWITH
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-016-434-1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAGAATGTCATCGGCATCCGAGACATTCTGCGGCGTCCACCCTGGAAGCCATGAGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTCTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGCCAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 ATGTATATATAGTACAGGACCTCATGGAAACAGATCTTTACAAGCTCTTGAAGACACAAC 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 Acarcecececececececes as a constant de la const
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                                              1081 AGGAGCGGCTGAAGGAGCTCATCTTCCAGGAGACAGCACGCTTCCAGCCCGGA
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35.2%; Score 646.6; DB 3; Length 1611;
Best Local Similarity 73.2%; Pred. No. 2.8e-124;
Matches 829; Conservative 0; Mismatches 304; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:blank
                                                                                                                                                                                                                                               Sequence 2, Application US/09412289

Sequence 2, Application US/09412289

Patent No. 6271210

GENERAL INFORMATION:

APPLICANT: Sivaraman, Vimala S.

APPLICANT: Mang, Haien-Yu

APPLICANT: Mang, Haien-Yu

TITLE OF INVENTION: ANTERNEE OLIGONUCLEOTIDES FOR MITC

TITLE OF INVENTION: PROTEIN KINASES AS THERAPY FOR CANC

TITLE OF INVENTION: NUMBER: US/09/412,289

CURRENT APPLICATION NUMBER: US/09/412,289

CURRENT PAPLICATION NUMBER: US/09/412,289

EARLIER PILING DATE: 1997-08-12

EARLIER PILING DATE: 1997-04-01

EARLIER FILING DATE: 1997-04-01

EARLIER FILING DATE: 1997-03-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: APPLICATION NUMBER: US/08/827,520

SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4
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ORGANISM: Homo sapiens
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1286 GTGACGAGCCCATCGCCGAAGCACCATTCAAGTTCGACATGGAATTGGATGACTTGCCTA 1345
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                                           806 CCTGTGATCTCAAGATCTGTGACTTTGGCCTGGCCCGTGTTGCAGATCCAGACCATGATC
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Sequence 1263, Application US/09016434
Sequence 1263, Application US/09016434
Sequence 1263, Application US/09016434
Settle No. 650033
Settle Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
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Pred. No. 2.7e-123;
0; Mismatches 270; Indels
           NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1263:
SEQUENCE CHARACTERISTICS:
IENGTH: 2791 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
LIBRARY: GENBANK
US-09-016-434-1263
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34.9%;
31 Similarity 74.9%;
804; Conservative
ATTORNEY/AGENT INFORMATION:
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cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-623-108-7
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US-10-623-108-3
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Maximum Match 100%
Listing first 45 summaries
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	Sequence 5, Application US/10623108 Sequence 5, Application US/10623108 Sequence 5, Application US/10623108 Sequence 5, Application US/10623108 SEQUENCE 10 No. US20050013817A1 APPLICANT: DAI, KEN-SHWO TITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH FILE REFERENCE: U 0.44726-8 CURRENT APPLICATION NUMBER: US/10/623,108 CURRENT PILING DATE: 2003-07-18 SOFTWARE: Patentin version 3.1 TYPE: DNA OGANISM: Homo sapiens -10-623-108-5 LENGTH: 1837 TYPE: DNA OGANISM: Homo sapiens -10-623-108-5 LENGTH: 1837; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 1837; Conservative 0; Mismatches 0; Indels 0; Gaps	ALIGNMENTS  Sequence 5, Application US/10623108 Sequence 5, Application US/10623108 Sequence 5, Application US/10623108 Sequence 5, Application US/10623108 APPLICANT: DAI, KEN-SHWO TITLE OF INVENTIONS: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH FILE REFERENCE: U 044726-8 CURRENT APPLICATION NUMBER: US/10/623,108 CURRENT PILING DATE: 2003-07-18 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PARENTIN VERSION 3.1 TYPE: DNA ORGANISM: HOMO Sapiens 100.0%; Score 1837; DB 8; Length 1837; TYPE: DNA ORGANISM: HOMO Sapiens 1 GAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	44 312.4 17.2 2187 8 US-10-278-698-701 Sequence 701, A 44 312.4 17.0 1502 5 US-10-197-315-1 Sequence 701, A 45 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 45 312.4 17.0 1502 5 US-10-197-315-1 10-623-108-5 Sequence 5, Application US/10623108 ALIGNMENTS Sequence 5, Application US/10623108 ALIGNMENTS DAI, KEN-SHWO PILE REPREMENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH FILE REPREMENT PILING DATE: 2007-18 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn version 3.1 SEQ ID NO S SEQ ID NOS: 8 SEQ ID NOS: 8 CURRENT FILING DATE: 2003-07-18 NUMBER OF SEQ ID NOS: 8 LENGTH: 1837 CREANISM: Homo sapiens 10-623-108-5 DATE: 00.0%; Score 1837; DB 8; Length 1837; Best Local Similarity 100.0%; Pred. No. 0; Matches 1837; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GAGGAGTGGAGATGGCGGGGGGGGGGGGGGGGGGGGGGG	41 320.4 17.4 3309 8 US-10-72-860-6956 Sequence 6956, 42 316.2 17.2 2187 8 US-10-278-699-185 Sequence 701, A 4 316.2 17.2 2187 8 US-10-278-699-185 Sequence 701, A 4 312.4 17.0 1502 5 US-10-198-343-1 Sequence 701, A 5 312.4 17.0 1502 5 US-10-198-343-1 Sequence 1, App 1.0 43-108-5 Sequence 1, App 1.0 5 Sequence 1,	0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-144-6494-456 0-1991-995-22034 0-1991-995-22034 0-1991-995-22034 0-1991-995-22034 0-1995-22034 0-1991-995-22034 0-1991-995-22034 0-1991-995-22034 0-1991-995-22034 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0-1901-14213 0	CACGCAGTTGCAGTACATCGGCGAAGGGCGCGTACGGC	erececceecer	121
Oy 121 ACGTGGGCCCGCGCTACACGCACTTGCAGTACATCGGCGAGGGCGCGTACGGCATGGTCA 180	TITLE OF INVENTION: 4020050013817A1  3ENERAL INFORMATION: 4020050013817A1  3ENERAL INFORMATION: 4020050013817A1  3ENERAL INFORMATION: 4020050013817A1  3ENERAL INFORMATION: 400AN SWAPK3-RELATED GENE VARIANTS ASSOCIATED WITH THE OF INVENTION HUMBER 10 10 10 10 10 18  CURRENT FILING DATE: 2003-07-18  SOFTWARE: Patentin version 3.1  SEQ ID NO 5  LENGTH: 1837  TYPE: DNA  ORGANISM: Homo sapiens  100-623-108-5  Duery Match  1 GAGGAGTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ALIGNMENTS  ALIGNMENTS  Sequence 5, Application US/10623108  Publication No. US20050013817a1  Sequence 5, Application US/10623108  Publication No. US20050013817a1  APPLICANT: DAI, KEN-SHWO  TITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH CAFFILE REFERENCE: U0.4726-8  CURRENT FILING DATE: 2003-07-18  CURRENT FILING DATE: 2003-07-18  CURRENT FILING DATE: 2003-07-18  SOFTWARE: Patentin version 3.1  SEQ ID NO 5  LENGTH: 1837  TYPE: DNA  ORGANISM: Homo sapiens  10.623-108-5  Duery Match  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1837; Conservative 0; Mismatches 0; Indels 0; Gaps  Matches 1837; Conservative 0; Mismatches 0; Indels 0; Gaps  1 GAGGAGTGGACATGGCGGCGCGCGCGCGCGGGGGGGGGG	44 312.4 17.2 2187 8 US-10-278-698-701 Sequence 701, A 4 312.4 17.0 1502 5 US-10-198-313-1 Sequence 1, App 4 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 3 12.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 3 12.4 17.0 US-10623108 Sequence 5. Application US/10623108 Sequence 5. Application No. US20050013817A1 TILLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH 7 TILLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH 7 TILLE OF INVENTION HUMBER: US/10/623,108 Seguence 5 Seguence 5. Seguence 5. Seguence 5. Seguence 5. Seguence 7. Seguence 7. Seguence 7. Seguence 8. Seguence 9. Seguence 9. Seguence 9. Seguence 9. Seguence 9. Seguence 9. Matches 1837; Conservative 0. Mismatches 0. Indels 0. Gaps 1. Seguence 1837; Conservative 0. Mismatches 1837; Conservative 1. Seguence 1837; Conservative 1837; Conservative 1. Seguence 1837; Conservative 1837; Conservative 183	41 320.4 17.4 3309 8 US-10-7278-6956 Sequence 6956, 443 316.2 17.2 2187 8 US-10-7278-698-105 Sequence 185, A 43 316.2 17.2 2187 8 US-10-278-698-701 Sequence 701, App 44 312.4 17.0 1502 5 US-10-198-343-1 Sequence 1, App 5 Sequence 1, App 12.4 17.0 1502 5 US-10-197-315-1 Sequence 2, Application No. US-20050013817Al SERERENCE UD 04.4726-8 CURRENT PRILE REFERENCE: U 04.4726-8 CURRENT PRILE REFERENCE: U 04.4726-8 CURRENT PRILE SEQUENCE: U 04.4726-8 CURRENT PRILE SEQU	9-854-133-456 0-144-649A-456 0-144-649A-456 0-144-649A-456 0-144-649A-456 0-144-649A-456 0-144-649A-456 0-264-049-1992 0-264-049-1992 0-395-22034 0-395-22034 0-396-22034 0-468-886-1 0-468-886-1 0-455-114-18739 0-455-114-18739 0-425-114-18739 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-42	gggggtcccggggaggtggagatggtgaaggggcag 	aaggggrcggcc 	61
61 CCGAGGGGGCCCGGGGGGGAGGTGGAGGTGAAGGGGCGTTCG	FULT 1  10-623-108-5  Sequence 5, Application US/10623108  Sequence 5, Application US/10623108  Sequence 5, Application US/10623108  SPLDIS REPROBREL INFORMATION:  APPLICANT: DAI, KEN-SHWO  TITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH  THIER SEREBREE: 10 10 14726-8  CURRENT FILING DATE: 2003-07-18  CURRENT FILING DATE: 2003-07-18  CURRENT FILING DATE: 2003-07-18  SOFTWARE: PatentIn version 3.1  SEQ ID NO 5  LENGTH: 1837  TYPE: DNA  ORGANISM: Homo sapiens  -10-623-108-5  Query Match  Beet Local Similarity 100.0%; Pred: No. 0;  Matches 1837; Conservative 0; Mismatches 0; Indels 0; Gaps	ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  10-623-108-5  Sequence 5, Application US/10623108  Publication No. US20050013817A1  APPLICANT: DAI. KEN-SHWO  TITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH  THE REPERENCE: U 014726-8  CURRENT PILING DATE: 2003-07-18  CURRENT FILING DATE: 2003-07-18  SOFTWARE: PatentIn version 3.1  SEQ ID NO 5  LENGTH: 1837  LENGTH: 1837  LENGTH: 1837  ONGAMISM: Homo sapiens  10-623-108-5  Query Match  Beet Local Similarity 100.0%; Pred. No. 0;  Matches 1837; Conservative 0; Mismatches 0; Indels 0; Gaps	44 312.4 17.2 2187 8 US-10-278-698-701 Sequence 701, A 4 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 4 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 32.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 32.4 17.6 17.2 17.2 17.2 17.2 17.2 17.2 17.2 17.2	41 320.4 17.4 3309 8 US-10-723-860-6556 Sequence 6956, 42 316.2 17.2 2187 8 US-10-278-698-185 Sequence 185, A 3 16.2 17.2 2187 8 US-10-278-698-101 Sequence 1701, A 12.4 17.0 1502 5 US-10-198-343-1 Sequence 1, App 44 312.4 17.0 1502 5 US-10-198-343-1 Sequence 1, App 5 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 6 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, App 7 17.0 1502 5 US-10-197-315-1 Sequence 1, App 8 17.1 Sequence 5, Application US/10623108 ALIGNMENTS  Publication No. US20050013817A1 APPLICANT: DAI, KEN-SHWO TITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH 7 ITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH 7 UNUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn version 3.1 SEQ ID NO 5 LENGTH: 1837 TYPE: DNA OKGAMISM: Homo sapiens -10-623-108-5 Duery Match 1837; Conservative 0; Mismatches 0; Indels 0; Gaps	9-854-133-456 0-144-649A-456 0-144-649A-456 0-144-649A-456 0-144-649A-456 0-264-049-1992 0-264-049-1992 0-998-22034 0-998-22034 0-998-22034 0-998-22034 0-998-01-22034 0-468-886-1 0-455-114-18739 0-455-114-18739 0-455-114-18739 0-425-114-18739 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-425-114-2624 0-4	GGCGGCGGCGGCTCAGGGGGGGGGGGGGGGGGGGGGGGCCCCCCCC	ggagtggagatgg             ggagtggagatgg	
1 GAGGAGTGGAGATGGCGGCGGCGGCGGGGGGGGGGGGGG	TITLE OF INVENTION:  TITLE OF INVENTION:  TITLE OF INVENTION:  TURBER APPLICATION:  APPLICANT: DAI, KEN-SHWO  TITLE OF INVENTION:  TOTHER OF INVENTION:  T	ALIGNMENTS  ALIGNMENTS  10-623-108-5  Sequence 5, Application US/10623108  Publication No. US20050013817A1  APPLICANT: DAI, KEN-SHWO  TITLE OF INVENTION:  THE REPERBENCE: U 014726-8  CURRENT APPLICATION NUMBER: US/10/623,108  CURRENT FILING DATE: 2003-07-18  NUMBER OF SEQ ID NOS: 8  SOFTWARE: PatentIn version 3.1  SEQ ID NO 5  LENGTH: 1837  TYPE: DNA  ORGANISM: Homo sapiens  -10-623-108-5	44 312.4 17.2 2187 8 US-10-278-698-701 Sequence 701, A 4 312.4 17.0 1502 5 US-10-198-31-1 Sequence 701, A 5 312.4 17.0 1502 5 US-10-197-315-1 Sequence 1, Applan 17.0 US-205-0013817A1 SEQUENCE 5 Application US/10623108 Sequence 5. Application No. US-205-0013817A1 SEPERAL INFORMATION: TRN-SHMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH PILE REFERENCE: U 014726-8 CURRENT FILING DATE: 2003-07-18 NUMBER: OF SEQ ID NOS: 8 SEQ UD NOS:	41 320.4 17.4 3309 8 US-10-723-860-6556 Sequence 6956, 42 316.2 17.2 2187 8 US-10-278-698-185 Sequence 185, A 43 316.2 17.2 2187 8 US-10-278-698-185 Sequence 1701, A 44 312.4 17.0 1502 5 US-10-198-343-1 5 312.4 17.0 1502 5 US-10-197-315-1  ALIGNMENTS  ALIGNM	2-44-133-456 2-44-649A-456 2-44-649A-456 2-44-640-49-1992 2-44-640-49-1992 2-44-660-49-1992 2-44-660-49-1992 2-44-660-49-1992 2-45-114-1992 2-45-114-1993 2-45-114-1993 2-45-114-1993 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-114-197 2-45-115-1 2-45-114-197 2-45-115-1 2-45-115-1 2-45-115-1 2-45-115-1 2-45-115-1 2-45-115-1 2-45-115-1 2-45-115-1 2-45-116-117-117-117-117-117-117-117-117-117	Score 1837; DB 8; Length 1837 Pred. No. 0; ; Mismatches 0; Indels 0	vat	Query Match Best Local Sim Matches 1837;
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146           7 320.4         17.4         286         US-10-425-114-26661         Sequence 246           8 320.4         17.4         2980         B US-10-737-450-105         Sequence 246           8 320.4         17.4         2980         B US-10-737-450-105         Sequence 286           9 320.4         17.4         3290         B US-10-723-860-2894         Sequence 286           1 320.4         17.4         3309         B US-10-737-860-2894         Sequence 266</td> <td>8 433.8         23.6         682         6 US-10-264-049-1992         Sequence 1999           9 416.6         22.7         641         7 US-10-404-460-74         Sequence 226           1 348.8         19.0         463         3 US-09-918-995-22034         Sequence 226           2 338.8         19.0         463         3 US-09-918-995-22034         Sequence 226           2 338.8         19.0         463         3 US-09-918-995-22034         Sequence 126           3 34         18.4         1396         8 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2863 8 US-10</td><td>494 26.9 574 5 US-10-144-649A-456 Sequence 433.8 23.6 682 6 US-10-264-049-1992 Sequence 22.7 682 6 US-10-264-049-1992 Sequence 238.2 21.7 544 3 US-10-918-995-2207 Sequence 238.8 19.0 463 3 US-10-918-995-2203 Sequence 238.8 18.4 1396 8 US-10-768-986-1 Sequence 338.8 18.4 1396 8 US-10-767-711-14213 Sequence 4325.4 17.7 1610 7 US-10-767-701-14213 Sequence 2320.4 17.4 2828 6 US-10-355-114-18739 Sequence 2320.4 17.4 2828 6 US-10-355-114-26261 Sequence 2320.4 17.4 2828 6 US-10-355-114-26261 Sequence 2320.4 17.4 2980 8 US-10-355-114-26261 Sequence 2320.4 17.4 2980 8 US-10-355-114-26261 Sequence 2320.4 17.4 2980 8 US-10-355-114-26261 Sequence</td><td></td><td>US-10-144-649A-456 US-10-26-049-1992 US-10-404-460-74 US-09-918-995-2207 US-09-918-995-22034 US-10-768-886-1 US-09-960-352-572 US-09-970-701-14213</td><td>0,00,00,00,00,00,00,00,00,00,00,00,00,0</td><td>27 494 28 43.8 29 416.8 30 398.2 31 348.8 32 348.8 33 35.4 34 325.4 36 320.4 40 320.4 41 320.4 42 316.2 43 316.2 44 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	RESULT 2 US-10-623-108-7 i Sequence 7. Application US/10623108 j Publication No. US20050013817A1 i GENERAL INFORMATION: j APPLICANT: DAI, KEN-SHWO j TILE REFERENCE: U 014726-8 j CURRENT PAPLIANIN: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS j CURRENT FILING DATE: 2003-07-18 j NUMBER OF SEQ ID NOS: 8 j SECTRARE: Patentin version 3.1 j SEQ ID NO 7 j LENGTH: 1777 j TYPE: DNA j ORGANISM: HOMO Sapiens US-10-623-108-7	Query Match   92.9%; Score 1707; DB 8; Length 1777;   Best Local Similarity   96.7%; Pred. No. 0;   Matches 1777;   Conservative   0; Mismatches   0; Indels   60; Gaps   1;   Matches 1777;   Conservative   0; Mismatches   0; Indels   60; Gaps   1;   GAGGAGTGGAGAGTGGGGGGGGGGGGGGGGGGGGGGG
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1501 GGCGCTGAGTAGGGGACTCAGGGCCATGCCTGCCCCCTCTCATTCAAACCCCCCT
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APPLICANT: 1ang, x. tom
APPLICANT: Liu, Chenghua
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Lowerman, Tom
APPLICANT: Jang, Jie
APPLICANT: Olan, Xiaohong B.
APPLICANT: Olan, Xiaohong B.
APPLICANT: Olan, Xiaohong B.
APPLICANT: Olang, Jie
APPLICANT: PUNGRIE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 3311
NUMBER OF SEQ ID NOS: 3311
NUMBER OF SEQ ID NOS: 3311
SECOTION NO. 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tang, Y. Tom APPLICANT: Tang, Y. Tom APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Asundi, Vinod APPLICANT: Zhou, Ping APPLICANT: Zhou, Ping APPLICANT: Zhou, Ping APPLICANT: Zhou, Ping APPLICANT: Chen, Yunding APPLICANT: Chen, Rei, Peryan APPLICANT: Wang, Zhiwei PPLICANT: Wang, Zhiwei PPLICANT: Weng, Zhiwei PPLICANT: Zhang, Jie PPLICANT: Chen, Xiaohong B. PLICANT: Drmanac, Radadam T. L. Chen, Xiaohong B. PLICANT: Drmanac, Radadam T. L. Chen, Xiaohong B. PLICANT: Drmanac, Radadam T. Chen, Yiaohong B. PLICANT: Drmanac, Radadam T. Chen, Xiaohong B. PLICANT: Drmanac, Radadam T. Chen, Xiaohong B. PLICANT: Drmanac, Radadam T. Chen, Yiaohong B. PLICANT T. Chen, Yiaohong B. PLICANT T. Chen, Yiaohong B. PLICAN
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GENE VARIANTS ASSOCIATED WITH CANCERS 1560 1449 1680 1209 1269 1440 1500 1620 1200 1321 GIGGAGCAIGGCCIGGCCACCICICTICCIGAGGCCICCAGCTICAGGCAGGCCA 1380 1329 1450 Geogergaseras de de contra de la 1509 de contra de contra de la 1509 de contra de contra de la 1509 de contra de contra de contra de la 1509 de contra de contra de contra de contra de la 1509 de contra del 1740 1140 GTGAGCAGAAGTGGAGCTGGGGGGGGTGGAGAGCCCGGCGCCCCTGCCACCTCCCTGACC 1800 GGCCGAATCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTGTTCTGTGTG 1570 GGCCGAATCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCTCGCTGCTTCTGTGTG AGGCCCCCTAGCCCAGACACATCTCTGCACCCTGGGGCCTGGAACAGAACTGGCAAAG TCAATCTCCCGCTGCTGCTGCTGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT GGCGCTGAGTAGGGACTCAGGGCCATGCCTGCCCCTCATCTCAAACCCCACCT -----cagreeceaeeaecerreacerreecareeaecreareaecra 1081 AGGCCCCCTAGCCCAGACATCTCTGCACCCTGGGGGCCT------AGGCCTTCTCCTCCCCACCCGCCCTCCCCACGGGCCTCGGGAGCTCAGGTGGCCCCAGT TCAATCTCCCGCTGCTGCTGCTGCCCTTACCTTCCCCAGCGTCCCAGTCTCTGGCAGT TCTGGAATGGAATGGGTTCTGGCTGCCCAACCTGCTGAAGGGCAGAGGTGGAGGTGGGG AGITITCCCTGAAGGAACATICCTIAGICTCAAGGGCTAGCAICCCTGAGGAGCCAGGCCG AGGAGCGCTGAAGGAGCTCATCCAGGACACAGCACCTTCCAGCCCGGAGTGCTGG CGTCTAATATATAAATATAGAGATGTGTCTATGGCTG 1726 CGTCTAATATATATATATAGAGATGTGTCTATGGCTG 1837 RESULT 5
US-10-623-108-1
; Sequence 1, Application US/10623108
; Publication No. US20050013817A1
; GENERAL INFORMATION:
APPLICANT: DAI, KEN-SHWO
; TITLE OF INVENTION: HUMAN SMAPK3-RELATED GE
; TICKENT APPLICATION NUMBER: US/10/623,108
; CURRENT APPLICATION NUMBER: US/10/623,108
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1654

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; Publication No. US20050221354A1
; GENERAL INFORMATION:
APPLICANT: Wyeth
; APPLICANT: Wounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Mon; TITLE OF INVENTION: Nucleic Acid Arrays for Mon; TITLE OF INVENTION: US/11/060,756
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1050
; LENGTH: 1400
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             Length 1654;
                                      0; Indels
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             Score 1451;
Pred. No. 0;
           79.0%;
             Query Match
Best Local Similarity 90.0
Matches 1654; Conservative
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APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Mon
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION WUMBER: US/11/060,756
CURRENT PILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
LENGTH: 1400
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NAME/KEY: misc feature
LOCATION: (1389)...(1389)
CTHER INFORMATION: n is a,
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             FEATURE:
NAME/KEY: misc feature
LOCATION: (1389)
COTHER INFORMATION: n is a,
US-11-060-756-1050
                                                                                                                                               Best Local Similarity 94.7
Matches 1333; Conservative
ORGANISM: Homo sapiens
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Sequence 38, Application US/10072036

| Sequence 38, Application WS/10072036
| Publication No. US2030082564A1
| Publication No. US2030082564A1
| Publication No. US2030082564A1
| APPLICAMT: Ole THASTRUP
| APPLICAMT: Soren TULLIN
| APPLICAMT: Soren TULLIN
| APPLICAMT: Kasper ALMHOLT
| APPLICAMT: Kasper ALMHOLT
| APPLICAMT: Wasper ALMHOLT
| APPLICAMT: On A Method For Extracting Quantitative Information Relating To An ITTLE OF INVENTION NUMBER: 09/417,197
| FILE REFERENCE: 3759-10-07
| PRIOR FILING DATE: 1999-10-07
| PRIOR FILING DATE: 1999-10-07
| PRIOR FILING DATE: 1996-10-07
| SEQ ID NO 38
| ERNGHT: 1896-10-07
| WUMBER OF SEQ ID NO 38
| ERNGHT: 1896-10-07
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                                 GTGGAGCTGGGGGGGGTGGAGAGCCCGGCGCCCTGCCACCTCCCTGACCCGTCTAATAT 1810
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Pred. No. 2.6e-308;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.9%;
Matches 1139; Conservative (
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; NAME/KEY: CDS
; LOCATION: (1)..(1893)
US-10-072-036-38
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US-10-072-036-38
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US-09-925-297-323
                                                        Query Match 58.6%;
Best Local Similarity 95.7%;
Matches 1137; Conservative
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Fatent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
FRIOR RILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05989
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 323
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ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-17
PRIOR PILING DATE: 2001-04-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 109
LENGTH: 1147
                                                                                                                                                                                                                                                                                                           Query Match 56.8%; Score 1043.2; DB 7; Length 1147; Best Local Similarity 94.7%; Pred. No. 1.1e-281; Matches 1115; Conservative 0; Mismatches 3; Indels 60;
                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                               .. (1078)
                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (1).
US-10-114-270-109
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APPLICANT: Bradigaru, Waleria
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Gamgolli, Baha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Gamean, Steacie J.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Ji, Weizhen
APPLICANT: Maderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, John R.
APPLICANT: Rastelli, John R.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, GO/281,086
RICH ROTHER APPLICATION NUMBER: GO/281,136
RRICH RILING DATE: 2001-04-05
RRICH RELING DATE: 2001-04-06
RRICH RILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Same
                                                                                                                                CATTCAAACCCCACCCTAGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATC 1663
                                                                                                        CCTGAGGAGCCAGGCCGGGAGCCCCTCCCTGTCAAAGCTGTCACTTCGCGTGCCCT 1723
                                                 937 CATTCAAACCCCCACCCTAGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGCTAGCATC 996
                                                                                                                                                                                                                                                                      Sequence 109, Application US/10114270 Publication No. US20040030110A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu, Ziāohong
Gusev, Vladimir Y.
Li, Li
Vernet, Corine
Zerhusen, Bryan D.
Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                          1664
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APPLICANT:
APPLICANT:
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781 CTGGGCTCCCCATCCCAGGAGCTGAATTGTATCATCAACATGAAGGCCCGAAACTA	Oy 194 CCACGTGCGCAN	CACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTGGAACATCAGACCTA 253
dy BSZ CIACAGICICICCAAAACCAAAGIGACIIGASCAAASCIIIICCCAAAICAAAC 211	254	31
912 TCCAAAGCCCTTGACCTGCTGGACCGGATGTTAACCTTTAACCCCAATAAACGGATCACA 97	246	. CGCTGAGGGAGATCCAGATCTTGCTGCGGATTCCGCCATGAGAATGTTAT 305 18.08.18.18.18.18.18.18.18.18.18.18.18.18.18
Db 901 TCCAAAGCCCTTGACCTGGTGCGGATGTTAACCTTTAACCCCAATAAACGGATCA 958 Oy 972 GTGGAGGAAGCGCTGGCTCACCTGGAGGAGTACTATGACCCGACGATGATGAGCC		
959	374	r (
П	Db 366 TCAGGACCTCA Ov 434 CCATATCTGCT	. IGGAGACAGACCTGTACAAGCTGCTTAAAAGCCAGCAGCAGCTGAGCAATGA 425 ACTTCCTCTACCAGATCCTGCGGGGCCTCAAGTACATCCACTCCGCGAA 493
115	426	
1021	494	CGTGCTCCACCAGAGATCTAAAGCCCTCCAACCTGCTCAACACCACCTGCGACCTTAA 553
Oy         1152         CCCAGACAGCTCTCTGCACCCTGGAGCTGGACG         1189           Db         1081         CCCAGACAGACATCTCTGCACCCTGGGGCTTGGACCTG         1118	Oy 554 GATTTGTGATT	CACCGCTTCCT 61
RESULT 11 US-10-072-036-56	614	
; Sequence 56, Application US/100/2036 ; Publication No. US20030082564A1	Db 606 GACGGAGTATG	
; GENERAL INFORMATION: ; APPLICANT: Sara BJRON ; APPLICANT: Sara BJRON . APPLICANT: Soren THILIN	Oy 674 CTATACCAAGT	CTATACCAAGTCCATGACATCTGGTCTGTGGGCTGCATTCTGGCTGAGATGCTCTCTAA 733 
22	An I Db 726 CCGGCCATCT Db 726 CCGGCCCATCT	COGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACATTCTGGGCATCCT 793 
	Oy 794 GGGCTCCCCAT	GGGCTCCCCATCCCAGGAGCTGAATTGTATCATCAACATGAAGGCCCGAAACTACCT 853 
,	8 8 8 8 4 8 4 8 4 8 4 8 4 8 8 4 8 8 4 8 8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ACAGTETETGCCTCCAAGACCAAGGTGGCTTGGGCCAAGCTTTTCCCCAAGTCAGACTC 913
; SEQ ID NO Se ; TYPE: DNA ; ORGANISM: Artificial Sequence	914	CAAAGCCCTTGACCTGGACCGGATGTTAACCTTTAACCCCAATAAACGGATCACAGT 973
; FEATURE: ; OTHER INFORMATION: mERK1-F64L-S65T-GFP fusion ; FEATURE:	974	
; NAME/KRX: CDS ; LOCATION: (1)(1872) US-10-072-036-56	Db 966 AGAGGAAGCGC	ÍTGGCTCACCCTTACCTGGAACAGTACTACGATCCGACAGATGAGCCAGT 1025 CCCTTCACCTTGGCCATGGAGCTGGATGACCTACCTAAGGAGCGGCTGAA 1093
Query Match 52.2%; Score 958.6; DB 5; Length 1875; Best Local Similarity 90.0%; Pred. No. 6.2e-258; Matches 114: Indels 0: Gaps 0;	1026	e :
14 GCGGCGCGCGCGCGCTCAGGGGGCGGGGGGGGGGGGGGG	Oy 1094 GGAGCTCATCT             Db 1086 GGAGTTGATCT	GGAGCTCATCTCCAGGAGACAGCACGTTCCAGCCGGAGTGCTGGAGGCCCCTAGCC 1153
50500	Oy 1154 C 1154	
DD 66 CCCGGTGGTCCCCGGGGAGGTGGTGAAGGGGCGAGCCATTCGATGTGGCCCACG 125		
OY 134 CTACACGCAGTTGCAGTACATCGGCGAGGCGCGTACGGCATGGTCAGCTCGGCCTATGA 193	RESULT 12 US-10-171-311-126 ; Sequence 126, Application US/101713: ; Publication No. US20030087270A1	ion US/10171311 0087270A1

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1226 AGAGGATTGAAGTAGAACAGGCTCTGGCCCACCCATATCTGGAGCAGTATTACGACCCGA 1285
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                                         TGAATTCCAAGGGCTACACCAAGTCCATTGATATTTGGTCTGTAGGCTGCATTCTGGCAG
                                                                                                                                                                                                                                                                                                                                                                       986 AAATGCTTTCCAACAGGCCCATCTTTCCAGGAAGCATTATCTTGACCAGCTGAATCACA
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601 ACACCGGCTTCCTGACGGAGTATGTGGCTACGCGCTGGTACCGGGCCCCAGAGATCATGC
                                                                                                                                                                                                                                                                                                                         AGATGCTCTCTAACCGGCCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACA
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Srephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION NUMBER: US 40/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2002-05-05
PRIOR APPLICATION NUMBER: US 60/381,978
PRIOR PILING DATE: 2002-05-05
PRIOR PILING DATE: 2002-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
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US-10-301-822-114
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                                                          APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Monahan, John
APPLICANT: Monahan, John
APPLICANT: Manakar, Shubhangi
APPLICANT: Manavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Goren, CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REPERENCE: MI-035
FILE REPERENCE: MI-035
FRIOR APPLICATION NUMBER: US 60/298,159
FRIOR APPLICATION NUMBER: US 60/298,155
FRIOR APPLICATION NUMBER: US 60/335,936
FRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCGAGGGGTCGGCCCGGGGGTCCCCGGGGAGGTGGAGATGGTGAAGGGGCAGCCGTTCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ACGIGGCCCCCCCTACACCCCAGITGCAGIACAICGGCGAGGGCGCGIACGCCAIGGICA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GCTCGGCCTATGACCACGTGCGCAAGACTCGCGTGGCCATCAAGAAGATCAGCCCCTTCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 GCTCTGCTTATGATATGTCAACAAGTTCGAGTAGCTATCAAGAAAATCAGCCCCTTTG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACATCAGACCTACTGCCAGCGCACGCTCCGGGAGATCCAGATCCTGCTGCGCTTCCGCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 ACCTCAGCAATGACCATATCTGTTTTTCTCTAACCAGATCCTCAGAGGGTTAAAATATA 745
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Pred. No. 1.6e-170;
0; Mismatches 304; Indels
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73.2%;
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Best Local Similarity 73.23
Matches 829; Conservative
                                         APPLICANT: Schlegel, Robert
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CRGANISM: Homo sapiens
US-10-171-311-126
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Best Local Similarity 74.9%;
Matches 804; Conservative 0
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                                                                         RESULT 14
US-10-305-720-1263
                                                                                                                                                                                                                        LENGTH: 2791
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Length 1611;
                    Indels
35.2%; Score 646.6; DB 6; 73.2%; Pred. No. 1.6e-170; iive 0; Mismatches 304;
                    Conservative
           Similarity
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APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression FILE REPERRINGE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR PILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PELL Program
SEQ ID NO 1263
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; OTHER INFORMATION: GenBank ID No. US20040010136A1 g23878
US-10-305-720-1263
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Pred. No. 3.6e-169;
0; Mismatches 270;
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                                                       GATGTCTACATTGTGCAGGACCTGAGGAGCTGACCTGTACAAGTTGCTGAAAAGCCAG
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Job time : 1587.19 secs
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APPLICANT: AZIZ, NALASHA
APPLICANT: Zlochik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFRENCE: £ile
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT APPLICATION BATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SEQ ID NO 513
LENGTHAR: 2791
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                                                                                            GAGATGCTCTCTAACCGGCCCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCAC
                                                                                                                                                         ATTCTGGGCATCCTGGGCTCCCCATCCCAGGAGGACCTGAATTGTATCATCAACATGAAG
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                                 CTGAACTCCAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTCTGGCT
                                                   AAACGGATCACAGTGGAGGGAAGCGCTGGCTCACCCTACCTGGAGCAGTACTATGACCCG
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Pred. No. 3.6e-169;
0; Mismatches 270;
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82.10-75-6-149-513
Sequence 513, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION
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CORGANISM: Homo Sapiens
US-10-756-149-513
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114, App 421, App 2601, App 10, App 11, App 1317, Ap 4959, Ap 1317, Ap 6879, Ap 6879, Ap

Sequence 1882, Sequence 107, A Sequence 154, A Dy Sequence 154, A Dy Sequence 2, App Sequence 421, A Sequence 10, Apj Sequence 10, Apj Sequence 1117, A Sequenc

154, App 6, Appli 2, Appli

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publication No. US20050266420A1

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: BYMMANS, W. FRASER

APPLICANT: HESS, KENNETH R.

APPLICANT: STEC, JAMES

APPLICANT: STEC, JAMES

TITLE OF INVENTION MULTIGANE PREDICTORS OF RESPONSE TO CHEMOTHERAPY

TITLE REFERENCE: UTXC: 880US

CURRENT APPLICATION NUMBER: US/10/955,054A

CURRENT APPLICATION NUMBER: 2004-09-30

NUMBER OF SEQ ID NOS: 195

SOFTWARE: PARGHIN Ver. 2.1

SEQ ID NO S.
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US-11-024-959-6
US-11-024-959-2
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Best Local Similarity 97.0%;
Matches 1783; Conservative
TYPE: DNA ORGANISM: Homo sapiens
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2485, Ap
2850, Ap
25, Appl
3928, Ap
3928, Ap
3928, Ap
3508, Ap
3608, Ap
3608, Appl
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1936.698 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
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3: /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/NSOB NEW PUB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USOB NEW PUB.seq:*
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                                         GenCore version 5.1.7
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US-11-136-527-284
US-11-136-527-114
US-11-136-527-1988
US-11-136-527-2485
US-11-136-527-2485
US-10-770-726-25
US-10-909-125-861
US-11-136-527-3928
US-11-136-527-3928
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US-LIL-186-ZBH-114,
Sequence 114, Application US/11186284
Fublication No. US200502664931
GENERAL INFORMATION:
APPLICANT Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Manahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: MONAHAN: US/11/186, 284
CURRENT FILING DATE: 2002-07-21
PRIOR FILING DATE: 2002-11-21
PRIOR PELICATION NUMBER: US 60/361, 978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SUGTAMER: FastSEQ for Windows Version 4.0
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APPLICANT: Wouth
APPLICANT: Wouth
APPLICANT: Wouth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
SOFTWARE: Patentin version 3.2
SEQ ID NO 1988
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Pred. No. 2e-135;
4; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1988, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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74.5%;
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Best Local Similarity 74.5'
Matches 788; Conservative
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US-11-136-527-1988
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                                                                                                                                              Length 1611;
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                                                                                                                                              35.2%; Score 646.6; DB 8; 73.2%; Pred. No. 4.6e-139; ive 0; Mismatches 304;
                                                                                                                                                                                                 Matches 829; Conservative
                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (328)...(1410)
US-11-186-284-114
ORGANISM: Homo Sapiens
                                                                                                                                                Query Match
Best Local Similarity
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US-11-136-527-2850
US-11-136-527-2850
Squence 2850, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of FILE REFERENCE: 031896-041000 (AM101086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGAGTGCTGGAGGCCCCTAGCCCAGA 1157
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Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: 1010086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830

SOSTWARE: PatentIn version 3.2
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Pred. No. 9.1e-54;
0; Mismatches 425; Indels 2
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US-11-136-527-2485
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APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
CURRENT APPLICATION NUMBER: US/10/770, 726
CURRENT APPLICATION NUMBER: US/10/770, 726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
629 TACGCGCTGGTACCGGGCCCCAGAGATCATGCTGAACTCCAAGGGCTATACCAAGTCCAT
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Pred. No. 2.5e-53;
0; Mismatches 438;
                                                                                                                                                                                                                                                                       Sequence 25, Application US/10770726 Publication No. US20050266409A1 GENERAL INFORMATION:
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56.5%;
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; ORGANISM: Homo sapiens
US-10-770-726-25
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11; Mismatches 372;
     CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2850
LENGTH: 3132
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; ORGANISM: Rattus norvegicus
US-11-136-527-2850
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                                                                                                                                                                                                                                       APPLICANT: Wyeth
APPLICANT: Worth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARS: Patentin version 3.2
SEQ ID NO 3828
LENGTH: 1665
                                                                                                                                                    CTACATTGTGCAGGACCTGATGGAGACTGACCTGTACAAGTTGCTGAAAAGC---CAGCA
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Pred. No. 2e-50;
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60.5%;
                                                 Matches 465; Conservative
Best Local Similarity
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                                                                       710 GGACATCTGGTGTGGGCTGTATCATGGCAGAGATGCTGACAGGGAAAAACTCTGTTCAA
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APPLICANT: Vickers, Timothy
APPLICANT: Wickers, Timothy
APPLICANT: Wolver, Timothy
APPLICANT: Koller, Erich
APPLICANT: Swayze, Eric
APPLICANT: Swayze, Eric
APPLICANT: Swayze, Eric
APPLICANT: Jain, Ravi
APPLICANT: Bat, Balkrishen
APPLICANT: Peralta, Eigen
TITLE OF INVENTION: Oligomeric Compounds And Comprise of Invention: ISISO080-100 (COREO016US)
TITLE OF INVENTION: Oligomeric COMPOUNDS AND FILE REFERENCE: 151S0080-100 (COREO016US)
TITLE OF INVENTION: OLIGOMER: US 60/492,056
PRIOR PLILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/516,303
PRIOR PLILING DATE: 2003-10-19
PRIOR PLILING DATE: 2003-12-19
PRIOR PLILING DATE: 2003-12-19
PRIOR PLILING DATE: 2003-12-19
PRIOR PLILING DATE: 2003-12-19
PRIOR PLILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 2184
SOFTWARE: FRAEESQ for Windows Verbion 4.0
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APPLICANT: Lollo, Bridget
APPLICANT: Bennett, C. Frank
APPLICANT: Freier, Susan M.
APPLICANT: Griffey, Richard H.
APPLICANT: Baker, Brenda F.
APPLICANT: Vickers, Timothy
APPLICANT: Marcusson, Eric G.
APPLICANT: Koller, Erich
APPLICANT: Swayze, Eric
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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 7924
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Pred. No. 2.6e-42;
                                                                                                                                                                                                                                                                                                        Sequence 7924, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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53.5%;
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; ORGANISM: Rattus norvegicus
US-11-136-527-7924
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Best Local Similarity 53.5
Matches 552; Conservative
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                                                                                                                                                                                        24;
                                                                                                                             Length 1665;
                                                                                                                         Score 233; DB 8; Length 16 Pred. No. 4.1e-44; 0; Mismatches 480; Indels
                                                                                                                      cch 12.7%;
al Similarity 53.3%;
575; Conservative
                                norvegicus
                                                                                                                         Query Match
Best Local Similarity
Matches 575; Conserv
TYPE: DNA ORGANISM: Rattus
                                                              US-11-136-527-3828
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APPLICANT: Wyeth
APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICATION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031895-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-05
SOFTWARE: Patentin version 3.2
SSQ ID NOS: 362830
SSEQ ID NOS: 362830
                     GCCCGGATTGCCGATCCTGAGCATGACCACACCGGCTTCCTGACGGAGTATGTGGCTACG
                                                                                                                                                       633 CGCTGGTACCGGGCCCCAGAGTCATGCTGAACTCCAAGGCTATACCAAGTCCATCGAC
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Pred. No. 6.2e-29;
0; Mismatches 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.1%;
Best Local Similarity 56.8%;
Matches 349; Conservative (
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US-11-136-527-3508
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Sequence 2977, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031980-041000 (AMI01086)

CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 2977
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739 CCATCTTCCCTGGCAAGCACTACCTGGATCAGCTCAACCACATTCTGGGCATCCTGGGCT 798
                                                                                                                                                                                             caccccrccrcadactrrcracacaagcracacacacacacacacaagaacracarcaacaaga 705
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                                                                                                                                 CTCTGCCCTCCAAGACCAAGGTGGCTTGGGCCCAAGCTTTTCCCCCAAGTCAGACTCCAAAG
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 203.8; DB 8; Length Pred. No. 2.7e-37; 0; Mismatches 317; Indels
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56.5%;
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CRGANISM: Rattus norvegicus
US-11-136-527-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGACATCTCTG 1169
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1006 AGACAGCTCTG 1016
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Pred. No. 1.2e-28;
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Matches 344; Conservative
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US-11-136-527-7604
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US-11-136-527-7604
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APPLICANT: Wyeth

MULES, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26
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Pred. No. 1.1e-28;
0; Mismatches 332;
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US-11-136-527-238
US-11-136-527-238
Septication US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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Best Local Similarity 55.7%;
Matches 452; Conservative
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COGANISM: Rattus norvegicus
US-11-136-527-238
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                                       ATGCTCTCTAACCGGCCCATCTTCCCTGGCAGCACTACCTGGATCAGCTCAACCACATT 782
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APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Gene

FILE REFERENCE: 031896-041000 (AMI01086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 4380

LENGTH: 600
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OM protein - protein search, using sw model

6, 2006, 15:19:31; Search time 266.938 Seconds (without alignments) 551.408 Million cell updates/sec February on:

Run

US-10-623-108-2 Perfect score:

1763 1 MAAAAAQGGGGEPRRTEGV.....LKELIFQETARFQPGVLEAP 335 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2443163 segs, 439378781 residues Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* A_Geneseq_21:* 1: geneseqp198 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Human	Human	Abm82548 Human dia	Adw12901 Human SMA	_	Human	_		_		Adq37846 Human pho	_		Adz65036 Mitogen a	Aam40540 Human pol			Aag67439 Amino aci	_	Abu89742 Protein d	Human	Ado24425 Human PRO		Aaw85006 Erk1-gree
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# ALIGNMENTS

human; KPP; kinase; phosphatase; enzyme; cytostatic; anorectic; immunosuppressive; KPP-Antagonist; KPP-Agonist; gene therapy; autoimmune disorder; obesity; cancer. ADH48364 standard; protein; 335 AA. Human KPP protein SEQ ID NO:22. 25-MAR-2004 (first entry) ADH48364; ADH48364 

WO2004001008-A2. Homo sapiens. 31-DEC-2003.

21-JUN-2002; 2002US-0390652P. 15-JUL-2002; 2002US-0396196P.

19-JUN-2003; 2003WO-US019660.

(INCY-) INCYTE CORP.

Marquis JP, Baughn MR, Tran UK, Hafalia AJA, Kable AE; Emerling BM, Elliott VS, Lindquist EA, Richardson TW, Khare R; Swarnakar A, Lee SY, Ramkumar J, Chawla NK, Becha SD, Mason PM; Hawkins PR, Bulloch SA, Jin P, Bhatia U, Burrill JD, Lee S; Blake JJ, Ho A, Zheng W;

WPI; 2004-082489/08. N-PSDB; ADH48413. New human kinases and phosphatases (KPP) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional KPP e.g., cancer.

Claim 1; SEQ ID NO 22; 336pp; English.

The invention relates to novel isolated human kinases and phosphatases (KPP) polypeptides. A protein of the invention has cytostatic, anorectic, and immunosuppressive activity, and acts as a KPP-Antagonist, or KPP-Agonist. A polymuclectide of the invention may have a use in gene therapy. The polypeptide is useful for preparing a composition for

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diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional KPP e.g., autoimmune disorders, obesity or cancer. The sequences shown in ADH48343-ADH48391 represent KPP proteins of the invention.
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TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Panser IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart ER, Wingrove J, Vitt UA, Kirton ES;
SM, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzes
Shi X, Suarez CJ;
                                                                                                                                                           DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
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N-PSDB; ACN41202.
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S, Shi X,
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Peralta CH,
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human clasmostic and therapeutic polynucleotides (dithp) or polyneptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine of autoimmune/inflammatory disorder, developmental disorders, or disorder, neurological disorders, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concleules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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New diagnostic and therapeutic polymucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQDLMBTDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAAAAQGGGGGFPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1763; DB 8; Length 335; 100.0%; Pred. No. 5.2e-174; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                 Claim 27; Page; 190pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 335 AA;
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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polymeptides may be cused to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine of autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conditions may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                  Gietzen D;
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                                                                                                                                                                                                                                                                                                                                                                                  New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
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                                                                                                                                      Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geretin EH,
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page; 190pp; English.
                                    2002US-0410259P.
2002US-0410260P.
12-SEP-2003; 2003WO-US028227
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                                                                                                    (INCY-) INCYTE CORP
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S. Shi X,
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACN41200
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                                        12-SEP-2002;
12-SEP-2002;
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                                                                                                                          DNA purification; diagnosis; cancer; mitogen-activated protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel isolated polypeptide (I) comprising ar amino acid sequence selected from sequences comprising 135 or 359 ami acids (ADW12901 or ADW12903) or its fragments. The polypeptides and polymucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SWAPK3 gene in a mammal. The fragments of the polypeptides and polymucleotides can also be used as primers or probes. This sequence corresponds to the SWAPK3V1 variant
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100.0%; Pred. No. 5.2e-174;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 2; 55pp; English
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              ADW12901 standard; protein; 335
                                                                                                  Human SMAPK3V1 variant protein.
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                                                                                                                                                                                                                                                                                                                (DAIK/) DAI K.
                                                                                                                                                                       Homo sapiens.
                                                                      07-APR-2005
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                                          ADW12901;
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ADW12901
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Mitogen activating protein kinase ERK1
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                                                          AAW15506 standard; peptide; 379
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                                                                                                                                                                    (first entry)
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                                                                                                            AAW15506;
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AMN15506
AMN15506
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259 --ALDLIDRMLTFNPNKRITVERALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
                                                                                                        KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                        1 MAAAAAQGGGGGEPRTTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                      VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
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19-JUL-2000; 2000US-00623312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-0059334.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the human mitogen activated protein (WAP) kinase ERK1. Fragments of this sequence (such as AAW15501) are recognition esquences for the antibodies of the invention. The antibodies of the invention. The antibodies of the invention. The antibodies of the invention are 1gG type monoclonal antibodies (WAb) generated by using human ERK1 as an immunogen and are capable of binding to ERK1 at the binding to buman or rat MAP kinase ERK2. Or rat MAP kinase ERK1 at mammal control of the antibodies can be used for detecting or assaying MAP kinases. They can be used for detecting or assaying MAP kinases. They can be used for detecting or assaying MAP kinases. They can be used for dispassing MAP kinases. Such as cancerassociated diseases (e.g. brain tumour), metabolic dispasses (e.g. asthma, pollenosis, atopic dermatitis), central nervous dispasses (e.g. asthma, pollenosis, atopic dermatitis), central nervous system diseases (e.g. Alzheimer's disease, Parkinsonism, senile dementia) and bone/joint diseases (e.g. rheumatism). They can also be used to investigate the role of MAP kinases in-vivo and the mechanism of drug action. The antibodies specific for various types of MAP kinases. By using antibodies specific for various types of MAP kinase, the activity sensitivity to the exclusion of other species of MAP kinase
                                                                                                                                                                                                                                                                                            Antibody; MAP kinase; human; mitogen activated protein; lymphoid cell; recognition sequence; 1gg(; immunogen; rat; BRK2; hybridoma; spleen cell; MAP kinase-related disease; cancer-associated disease; brain tumour; metabolic disorder; diabetes mellitus; circulatory disease; rheumatism; arteriosclarosis; allexigic diseases; central nervous system disease; asthma; Alzheimer's disease; parkinson's disease; senile dementia; BRK1; bone/joint disease; pollenosis; atopic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies to human MAP kinase - used for the detection, assay and purification of various MAP kinase species.
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Wang D;
Zhao QA;
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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Wang J,
Zhou P,
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ij

Gaps

44;

Length 379; Indels

Query Match 98.2%; Score 1731; DB 2; Best Local Similarity 88.4%; Pred. No. 1.3e-170; Matches 335; Conservative 0; Mismatches 0;

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WO2003021225-A2
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                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and extostatic activity. The polymocleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and central nervous system disease, such as a localised neuropathies and central nervous system disease, such as alateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and therapy, drug screening, assaays for receptor activity, arthritis and inflammation, leukaemias and C. N. S disorders. Note: The sequence data for this patent did not form
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                      1 MAAAAAQGGGGEPRRTEGVGPGVFGEVERWYKGQPFDVGPRYTQLQYIGEGAYGWVSSAY
                                                                                                                                                                                                                                                                                                                                                                                 VQDLMETDLYKILKSQQLSNDHICYFLYQILRGLKYHSANVLHRDLKPSNLLINTTCDL
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                                                                                                                                                                                                                                                                                                0; Indels 44;
                                                                                                                                                                                                                                                                         Score 1731; DB 4; Length 379;
Pred. No. 1.3e-170;
                                   English.
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                   Example 3; SEQ ID NO 1899; 10078pp;
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88.4%;
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Best Local Similarity
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The invention relates to identifying an agent to be tested for ability to treat psychotic disorder in patient. The method involves contacting cells of tissues with a candidate drug, and determining levels of phosphorylation of intracellular signaling proteins DARPP-32 (dopamineregulated phosphoprotein), ERK1 and ERK2 (extracellular signal-regulated protein kinases 1 and 2), and CREB (CAMP-response element binding protein). The method is useful for identifying an agent to be tested for an ability to treat a psychotic disorder such as schizophrenia in a patient in need of such treatment. The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                 Identifying agent to be tested for ability to treat psychotic disorder, by contacting cells/tissues with candidate drug, determining phosphorylation levels of intracellular signaling proteins DARFP-32, ERK1, ERK2, CREB.
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Pred. No. 1.3e-170;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 77-78; 79pp; English.
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                                                                                                       31-AUG-2001; 2001US-0316338P
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Best Local Similarity 88.4%;
Matches 335; Conservative
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13-MAR-2003
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361 KELIFQETARFQPGVLEAP 379
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                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 --ALDLIDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
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                                                                                                                                                                                                                                                                             Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQY1GEGAYGMVSSAY
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0
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Pred. No. 1.3e-170;
0; Mismatches 0;
                                                        Human; protein kinase; enzyme; inhibitor; ERK1.
                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 19; 260pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.2%;
                                                                                                                                                           20-MAR-2003; 2003WO-US008725
                                                                                                                                                                                 21-MAR-2002; 2002US-0366892P
             (first entry)
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Best Local Similarity 88.4
Matches 335, Conservative
                                                                                                                                                                                                                                 Braisted
                                                                                                                                                                                                                                                        WPI; 2003-865136/80
                                   Human kinase ERK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 379 AA;
                                                                                                           WO2003081210-A2
                                                                                     Homo sapiens.
             12-FEB-2004
                                                                                                                                                                                                                                 Prescott JC,
                                                                                                                                   02-OCT-2003
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The present invention relates to identifying and obtaining a compound useful in the prevention or treatment of cardiac diseases, comprising quantification of the activity of Raf-1, MEX1/2 and/or Erk1/2 depending compound. The method is useful for identifying and/or obtaining compounds that may be used in the prevention or treatment of cardiac diseases, particularly congestive heart failure. The compound or protein is also used for the preparation of a pharmaceutical composition for prevention or treatment of a disease related to hypertrophy or impaired or increased activation of telethonin (T-Cap), kagri-actinin, MHC, actin, composition for a proponin, Erk1/2 and/or MLCK. The protein or antibody which specifically recognizes the activated/phosphorylated form of the above polypeptide, is used for the preparation of a composition for diagnosing a disease or a predisposition of composition for diagnosing a disease or a predisposition contration of Raf-1, MEX1/2 and/or Erk1/2. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying and/or obtaining a compound useful for preventing or treating cardiac diseases, particularly congestive heart failure, comprises quantification of the activity of Raf-1, MEX1/2 and/or Erk1/2 depending on the compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reuner B, Brinkmann K;
                                                                                                                                                                                                                                                                     cardiac disease; Raf-1; MEK1; Cardiant; telethonin; &agr-actinin;
hypertrophy; MEK2; Brk1; Brk2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leclair S, Funk M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 33; SEQ ID NO 8; 41pp; English.
ADH59632 standard; protein; 379 AA.
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24-SEP-2001; 2001US-0324625P.
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                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-371821/35.
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                                                                                                                                                                                                           Erkl protein.
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                       25-MAR-2004
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88.4%;

Local Similarity

us-10-623-108-2.rag

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This invention relates to a novel use of biochemical pathways for identifying a mammalian glioma tumour that is likely to respond to an epidermal growth factor receptor (EGFR) polypeptide inhibitor or an mTOR polypeptide inhibitor, or identifying a mammalian glioma tumour that does not express or expresses a PTEN polypeptide and which is likely to respond or not likely to respond to an inhibitor of mTOR polypeptide activity, respectively. The biochemical pathways are, in particular, disregulated in pathologies such as cancer. The present sequence is that of the human ERK protein which may be used in the method of the invention.
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                                                                                                                                                                                 SKALDLIDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 360
 180
              241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                 --ALDLIDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMBLDDLPKERL
                                                      KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an
                                                                                                                                                                                                                                                                                                                                                                                                                                biochemical pathway; mammalian glioma tumour;
epidermal growth factor receptor; EGFR; mTOR; polypeptide inhibitor;
cancer; ERK; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of biochemical pathways associated with glioblastoma for, e.g. identifying a mammalian glioma tumor that is likely to respond to epidermal growth factor receptor polypeptide inhibitor or an mTOR polypeptide inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALIFORNIA.
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8; Length 379;

98.2%; Score 1731; DB

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; HER-2 directed therapy; tumour; insulin growth factor receptor; IGFR; epidermal growth factor receptor; EGFR; S6 ribosomal protein; AKT; NDF; ERK; cancer therapy; predictive biomarker; HER-2/neu.
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQXIGEGAYGMVSSAY
                                                                                                                                                                               DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                             61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLRAMRDVYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ALDLLDRMLTFNPNKRITVBBALAHPYLEQYYDPTDBPVAEBPFTFAMBLDDLPKERL
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                              Gaps
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                              44;
                              Indels
Pred. No. 1.3e-170;
0; Mismatches 0;
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                              335; Conservative
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Matches
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/note= "phosphorylated"

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This invention relates to a novel method for determining or predicting the response of a patient to HER-2 directed therapy. Specifically, it refers to analysing a mammalian tumour in order to detect a pattern of expression and or phosphorylation of a protein taken from the group including insulin growth factor receptor (IGFR) polypeptide, epidermal growth factor receptor (EGFR), phosphorylated SG ribosomal protein, phosphorylated AKT, phosphorylated NDF or phosphorylated ERK protein. The present invention describes characterising a mammalian tumour's responsiveness to an HER-2 therapy and hence an individual's response to this cancer therapy, using an immunologically specific antibody directed against one of the aforementioned proteins. Furthermore, it provides therappeutic agents targeted to HER-2/neu. This polypeptide sequence is the human phosphorylated ERK protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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expression, phosphorylation or both, of one or more polypeptides
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                                                                                                                                                                                                                                                                                                                                                                   Length 379;
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                                                                                                                                                                                                                                                                                                                                                                   Score 1731; DB 8;
Pred. No. 1.3e-170;
0; Mismatches 0;
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204
                                  Claim 35; SEQ ID NO 3; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                    98.2%;
88.4%;
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                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.4
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                    Sequence 379 AA;
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The invention relates to a novel method for identifying a mammalian tumor responding to HER2-directed therapy, where the tumor overexpresses HER2. The method involves assaying a sample obtained from the mammalian tumor to detect a pattern of expression and/or phosphorylation of one or several polypeptide, exhibit receptor (EGFR) polypeptide, neu differentiation factor (NDF) polypeptide, net detected pattern of expression, phosphorylation or both expression and phosphorylation identifies mammalian tumors that respond to HER2-directed therapy. The method of the invention is useful for identifying a mammalian tumor that responds to a HER2-directed therapy, the method of the invention is useful for identifying a mammalian tumor that responds to a HER2-directed therapy, the method is useful for determining or molecule targeting HER2. The method is useful for determining or molecule targeting response to the method is useful for determining or present speediction of responds therapy in an individual. The method canables prediction of response in cancer subjects to cancer therapy. The present sequence represents the human ERK protein used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                   Identifying mammalian tumor responding to HER2-directed therapy, involves assaying sample from tumor to detect expression and/or phosphorylation of insulin-like growth factor receptor polypeptide/erbB1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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88.4%; Pred. No. 1.3e-170;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 35; SEQ ID NO 3; 21pp; English.
                                                                                                                                                                                                                                       (VENT-) VENTANA MEDICAL SYSTEMS INC. (CELL-) CELL SIGNALING TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRPIFPGKHYLDQLNHIL-----
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                                                                                                                                                            2002US-0370473P.
                                                                                                                   11-DEC-2003; 2003US-00735118
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Matches 335; Conservative
                                                                                                                                                                                                                                                                                                       Smith BL;
                                                                                                                                                                                                                                                                                                                                             2005-072808/08
                                                                                                                                                                                                                                                                                                                                                                REFSEQ; XP_055766
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                                     US2004248151-A1.
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                                                                                                                                                            05-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting phosphorylated mitogen activated protein kinase (P-MAPK), by contacting sample with antibody having affinity for P-MAPK, detecting antibody/P-MAPK complex to detect P-MAPK, and expression of P-MAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAAAAQGGGGGBPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
                 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP kinase; Mitogen-activated protein kinase; enzyme; cancer.
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Pred. No. 1.3e-170;
0; Mismatches 0; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitogen activated protein kinase, MAPK-3, SEQ ID 2.
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                                                                                                                                                                                                                                                                            KELIFOETARFOPGVLEAP 335
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88.4%;
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14-OCT-2003; 2003WO-US032248.
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REFSEQ; XP_055766.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKALDELDRAKTENPNKRITVEBALAHPYLEQYYDPTDEPVAEBFFTFAMELDDLFKERL 360
NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA purification; diagnosis; cancer; mitogen-activated protein kinase;
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                                            --ALDLLDRMLTFNPNKRITVBEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKBRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel isolated polypeptide (I) comprising a amino acid sequence selected from sequences comprising 335 or 359 am acids (ADW12901 or ADW12903) or its fragments. The polypeptides and polypucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal. The fragments of the polypeptides and polynucleotides can also be used a primers or probes. This sequence corresponds to the SMAPK3V1 variant
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llarity 88.4%; Pred. No. 1.3e-170;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 standard; protein; 379 AA
                                                                                                                                                     KELIFOETARFOPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                                                  Human SMAPK3V3 variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2003; 2003US-00623108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2003; 2003US-00623108
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hes 335;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosupplessant and cytochatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous injuries, peripheral nervous coalised neuropathy and localised neuropathies and central nervous system diseases, such as a linearies of the activities and shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
Example 2; SEQ ID NO 5471; 10078pp; English.
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, Zhao QA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humtington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                          KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 5471.
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25-ARR-2000; 2000US-00552317.
20-UJN-2000; 2000US-0059042.
19-UJL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653450.
19-CT-2000; 2000US-00653450.
29-NOV-2000; 2000US-00737344.
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vel nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.

WPI; 2001-442253/47. N-PSDB; AAI59696.

Novel

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKALDLIDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLFKERL
                                                                                                                                       25 MAAAAAGGGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                  44; Gaps
                                 Length 403;
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                               Score 1731; DB 4;
Pred. No. 1.4e-170;
0; Mismatches 0;
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                               Query Match 98.2%;
Best Local Similarity 88.4%;
Matches 335; Conservative (
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He : 274.438 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

February Run on:

6, 2006, 15:29:28; Search time 25.1009 Seconds (without alignments) 1284.124 Million cell updates/sec

Perfect score: Title:

US-10-623-108-2 1763 1 MAAAAAQGGGEPRRTEGV.....LKELIFQETARFQPGVLEAP Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl: pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

mitogen-activated protein kinase (EC extracellular sign mitogen-activated extracellular sign MAP kinase mpk-1 (MAP kinase sur-1 (pathogenicity MAP mitogen-activated protein kinase ERK mitogen-activated protein kinase (EC mitogen-activated protein kinase MMK extracellular sign protein kinase ERK MAP kinase 1 (EC 2 Ca2+/calmodulin-de Ca2+/calmodulin-de MAP kinase 3 (EC 2 Ca2+/calmodulin-de Description SUMMARIES A48082 JC1451 S28184 S280841 JW0052 S25011 JQ1400 JQ1400 JQ1400 JW0053 JW0053 A39754 A46036 A36978 751944 751944 751943 756042 815663 831663 833635 851321 851320 747803 B Query Match Length 811.9 811.4 811.4 811.3 811.3 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 772.1 1725 1656 1656 1636 1445.5 1444.5 1444.5 1444.5 1444.5 1444.5 1444.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 1447.5 144 808.5 808.5 803.5 803.5 803.5 Result No.

mitogen-activated	mitogen-activated	mitogen-activated	mitogen-activated	mitogen-activated	mitogen-activated,	protein T30E16.13	mitogen-activated	extracellular sign	hypothetical prote	probable serine/th	protein F14N23.9 [	hypothetical prote	protein kinase (EC	probable protein k	mitogen-activated
S56638	T14915	S40471	839559	T03971	S52989	F96619	S60121	B56708	C86214	A33297	F86236	C86146	S28548	T13024	S68675
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369	371	376	372	375	384	376	371	815	363	368	370	369	353	373	349
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799.5	79	7													

## ALIGNMENTS

RESULT 1  A48082  MAP kinase 3 (EC 2.7.1) - human  N;Alternate names: extracellular signal-regulated kinase 1 (ERK1); mitogen-activated prot  N;Contains: protein kinase (EC 2.7.1.37)  C;Species: Homo sapiens (man)  C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004  C;Accession: A48082; PO0270; S23428; S15519; S21579  R;Charset, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.  Mol. Cell. Biol. 13, 4679-4690, 1993  A;Title: Molecular cloning, expression, and characterization of the human mitogen-activat  A;Accession: A48082	A;Status: translation not shown A;Status: translation not shown A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-379 <chm> A;Cross-references: UNIPROT:P27361; UNIPARC:UPI0000035BE2; EMBL:X60188; NID:g31220; PIDN A;Experimental source: hepatoma call line HEP G2 A;Note: authors translated the codon AGC for residue 174 as 1le R;Owaki, H; Makar, R: Boulton, T.G.; Cobb, M.H.; Geppert, T.D. Biochem: Biophys: Res. Commun. 182, 1416-1422, 1992 A;Title: Extracellular signal-regulated kinases in T cells: characterization of human ERP A;Accession: PQ0270.</chm>	A; Generic GDB:PRKM3; ERK1 A; Cross-references: GDB:135679; OMIM:601795 A; Map position: 16pter-16qter C; Complex: monomer C; Complex: monomer C; Complex: monomer C; Punction: A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine C; Superfamily: kinase accade C; Superfamily: kinase related transforming protein; protein kinase homology C; Keywords: ATP; monomer; phosphorotein; phosphotransferase; serine/threonine-specific p F; 40-330/Domain: protein kinase homology <kin> F; 48-56/Region: protein kinase homology <kin> F; 48-56/Region: protein kinase ATP-binding motif F; 202/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted F; 204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status</kin></kin>
A; Status: translation not shown A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-379 < CCHA> A; Residues: 1-379 < CCHA> A; Cross-references: UNIPROT: P27361; UNIPARC: UPI0000035BE2; EMBL: X60188; NID: 931220; PIDN A; Cross-references: UNIPROT: P27361; UNIPARC: UPI0000035BE2; EMBL: X60188; NID: 931220; PIDN A; Coss-references: UNIPROT: P27361; UNIPARC: UPI0000035BE2; EMBL: X60188; NID: 931220; PIDN B; Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D. B; Oden: Biophys. Res. Commun. 182, 1416-1422, 1992 A; Title: Extracellular signal-regulated kinases in T cells: characterization of human ERI A; Reference number: JQ1400; MUID: 92171961; PMID: 1540184		

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A;Cross-references: UNIPARC:UPI0000170057; GB:S58470; NID:g236372; PIDN:AAB19973.1; PID:çC;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; calmodulin binding; phosphotransferase; protein kinase
A;Residues: 14-94,'R',96-380 <DEM>
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A; Residues: 7-16 < CRE>
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ACAGONICATE AND CAPEGORD REAL MANAGE SEXTRACELLULAR SIGNAL-requiated kinase
N.Alternate names: ERKI-NAP kinase; extracellular signal-requiated kinase
C.Species: Ratus norregicus (Norway rat)
C.Date: 30-Sep-1993 #sequence revision 31-Sep-1993 #text_change 09-Jul-2004
C.Date: 30-Sep-1993 #sequence revision 31-Sep-1993 #text_change 09-Jul-2004
R.Marquardt, B.; Stabel, S.
Gone: 120, 297-299, 1992
A.FILE: Sequence of a rat cDNA encoding the ERKI-MAP kinase.
A.Recession: JCL451; MUID: 93013050; PMID: 1327976
A.Anocession: JCL451; MUID: 93013050; PMID: 1327976
A.Anocession: JCL451; MUID: 93013050; PMID: 1327976
A.Anocession: JCL451
A.Recession: JC
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                                                                                                                                                                                                                                                   DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
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                                                                                                                                                         1 MAAAAAQGGGGGFPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY

    - ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL

                                                                                                       1 MAAAAQGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                     Gaps
                                                       44;
Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRPIFPGKHYLDQLNHIL-------
                                                  Indels
Score 1725; DB 1;
                      Pred. No. 1.8e-70;
                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 KELIFOETARFOPGVLEAP 379
97.88;
                         Best Local Similarity 88.1%;
Matches 334; Conservative
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  Query Match
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A,Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:g515498; PIDN:AAA2000 C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; calmodulin binding; phosphorotein; phosphotransferase; serine/threonine F;41-331/Domain: protein kinase homology KIN> F;449-57/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National integration process in Alianse (b. 4.)......) entry and incomplete the mouse (argument) for the mouse (by Alternate names: extracellular signal-regulated kinase 1 (species: Mus musculus (house mouse) (species: Mus musculus (house mouse) (space) and the mouse in a sequence revision 30-Jan-1998 #text_change 09-Jul-2004 (space) and the mouse in a sequence revision 30-Jan-1998 #text_change 09-Jul-2004 (space) and the mouse in a sequence revision 30-Jan-1998 #text_change 09-Jul-2004 (space) and the mouse extracellular signal regulated kinase (erk-1). A species on sequence number: S28184; MulD:93144347; PMID:8424957 (and the mouse and and the mouse and and the mouse and the mouse and the mouse and the mouse are particular analysis of microtubule-associated protein-2 kinase cDNA from mouse are analysis of microtubule-associated protein-2 kinase cDNA from mouse are analysis of mulD:91369479; PMID:1716439
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A,Molecule type: mRNA
A,Residues: 74-377 < LBN>
A,Residues: 74-377 < LBN>
A,Cross-references: UNIPARC: UPI0000023599, GB:S59517
R;Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.
Proc. Natl. Acad. SGI. U.S.A. 88, 8845-8849, 1991
A,Fitle: Mouse Erk-1 gene product is a seriae/threonine protein kinase that has the poter A,Reference number: A41371; MUID:92020947; PMID:1717989
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Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) erk-1 - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSN
                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                  Score 1656; DB 2; Length 380;
Pred. No. 2.1e-67;
1; Mismatches 10; Indels 4
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                                                                                                                                                                                                                             Query Match 93.9%;
Best Local Similarity 85.4%;
Matches 323; Conservative
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extracellular signal-regulated kinase (BC 2.7.-.-) 1 - common carp

NyAlternate names: CERKI

C;Species: Cyprinus carpio (common carp)

C;Accession: JW0052

R;Hashimoto, H: Yokoyama, Y: Matsuo, Y: Toyohara, H:; Kohno, M:; Sakaguchi, M:

J. Blochem. 123, 1031-1035, 1998

A;Title: Existence of two isoforms of extracellular signal-regulated kinase in fish.

A;Reference number: JW0052; MUID:98269030; PMID:9603989

A,Accession: JW0052

A,Accession: JW0052

A,Residues: 1-392 < HAS>

A;Residues: 1-392 < HAS>

A;Comment: This enrayme is the key enzyme in the intracellular signal transduction pathway

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: phosphotransferase

F;54-344/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                          250
                                                   240
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                                                                                         ----ALDLLDRM 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AAVAVGGANG-----AAGP-KPG-LESVKGONFDVGPRYTDLQYIGEGAYGMVCSAFDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 ALDLLDRMLTFNPNKRITVBEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKE
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                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82,6%; Score 1455.5; DB 2; Best Local Similarity 77.3%; Pred. No. 1.8e-58; Matches 286; Conservative 13; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIYEETARFO 386
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Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) ERK1 - Chinese hamster (fragment Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) ERK1 - Chinese hamster (Ga2+/calmodulin-dependent signal-regulated kinase 1 (ERK1); MAP kinase; microtubu C; Species: Cricetulus griseus (Chinese hamster)
C; Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C; Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C; Date: 03-Mar-1992
Mol. Biol. Cell 3, 63-71, 1992
A; Title: Punctional expression and growth factor activation of an epitope-tagged p44 mit A; Reference number: A60041; MUID:92199340; PMID:1372523
A; Accession: A60041
A; Residues: 1-369 *MEL>
A; Residues: 1-369 *MEL>
A; Residues: 1-369 *MEL>
C; Comment: This serine/threonine kinase is activated in response to extracellular stimul C; Superfamily: kinase-related transforming protein; protein kinase homology
C; Keywords: AFF; calmodulin binding; phosphoprotein; phosphotransferase; protein kinase F; 30-320/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                 VRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQ 122
                                                                                                                                                                                                                                          DLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKI 182
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                                                                                                                                       3 AAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDH
                                                                                                                                                                          AAAAPGGGGGEPRGTAGVVPVVPGEVEVVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDH
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                                                                                                 44;
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llarity 85.6%; Pred. No. 1.6e-66;
Conservative 2; Mismatches 7; Indels 4
                                                          Length 377;
                                                                                               Indels
                                                                                               10;
                                                          5;
                                                      Score 1655; DB 2;
Pred. No. 2.3e-67;
1; Mismatches 10
F;38-328/Domain: protein kinase homology <KIN>F;46-54/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIFQETARFQPGVLEAP 335
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                                                            93.9%;
85.4%;
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                                                          Query Match
Best Local Similarity 85.4
Matches 322; Conservative
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nes 316;
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NRPIFPGKHYLDQLNHIL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.9
Best Local Similarity 74.3
Matches 278; Conservative
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A;Molecule type: mRNA
A;Residues: 1-358 <HER>
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N.Alternate names: extracellular signal-regulated kinase

Cipacises: Bos primigenius taurus (cattle)

Cipate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

Cipate: 20-Feb-1995 #sequencing of ERKZ from a bovine adrenal medulla cDNA library

A.Feferance number: 825011

A.Referance number: 82501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRPRHENVIGIRDILRASTLEAMRDVYI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1445.5; DB
; Pred. No. 4.6e-58;
17; Mismatches 17
                                                                                                                                                                                                                                                                                                                    A.Residues: 1-360 <ELY>
A.Cross-references: UNIPROT:P46196; UNIPARC:UPIOO
C.Superfamily: Winase-related transforming protei
C.Keywords: ATP; phosphotransferase
F;23-313/Domain: protein kinase homology <KIN>
F;31-39/Region: protein kinase ATP-binding motif
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Best Local Similarity 74.6
Matches 279; Conservative
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A;Accession: $23426
A;Accession: $23426
A;Rolecule type: mRNA
A;Residues: 13-500 cGON1>
A;Cross-references: UNIPARC:UPI000016A28D; EMBL:Z11695; NID:g23878; PIDN:CAA77753.1; PID: A;Cross-references: UNIPARC:UPI000016A299; EMBL:Z11694; NID:g23880; PIDN:CAA77753.1; PID: A;Residues: 1-90, 'Q', 92-360 cGON2>
A;Residues: 1-90, 'Q', 92-360 cGON2>
A;Rolecule type: mRNA
A;Residues: 1-90, 'Q', 92-360 cGON2>
A;Cross-references: UNIPARC:UPI000016A299; EMBL:Z11694; NID:g23880; PIDN:CAA77752.1; PID: C;Coment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723). C;Genetics:
A;Genetics: A;G
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A;Note: part of this sequence was confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŭ
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N;Alternate names: cell division cycle-2-related protein kinase ERK2
C;Specias: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: S16444; S15015; PN0480
R;Her, J.H.; Wu, J.; Rall, T.B.; Sturgill, T.W.; Weber, M.J.
Nucleic Acids Res. 19, 3743, 1991
A;Title: Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by tyrosine
A;Reference number: S16444; MUID:91305126; PMID:1649458
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        Kriedne, D.W.; Kousboumnon, A.D.; Maillio, F.; Elickbon, A.K.; Her, D.H.; Shadahowicz, D. Raido J. 10, 885-892, 1991

A; Title: Identification of the regulatory phosphorylation sites in pp42/mitogen-activate A; Reference number: S15015; WUID:91184134; PMID:1849075

A; Reference number: S15015

A; Retains preliminary

A; Molecule type: protein

A; Residues: IT-181, X', 183-189 < PMY>

A; Molecule type: protein

A; Residues: UNIPARC: UP1000017558

R; Ershler, M.A.; Nagorskaya, T.V.; Visser, J.W.M.; Belyavsky, A.V.

Gene 124, 305-3106, 1993

A; Title: Novel CDC2-related protein kinases produced in murine hematopoietic stem cells.

A; Reference number: PN0479; MUID:93185941; PMID:8444355

A; Accession: PN0480

A; Status: nucleic acid sequence not shown

A; Molecule type: mRNA

A; Residues: 145-195 < RES>

A; Cross-references: UNIPARC: UP10000175589

C; Keywords: ATF; cell cycle control; phosphoprotein; phosphotransferase; serine/threonin F; 21-31/Oomain: protein kinase homology < C; Keywords: ATF; cell cycle control; phosphoprotein; phosphotransferase; serine/threonin F; 181/Oomain: protein kinase ATF-binding motif

F; 183/Binding site: phosphate (Thr) (covalent) #status experimental

F; 185/Binding site: phosphate (Tyr) (covalent) #status experimental
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protein kinase (EC 2.7.1.37) ERK2 - rat
C;Species: Ratus norvegicus (Norvay rat)
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
C;Accession: A40033
R;Boulton, T.G.; Nye, S.H.; Robbins, D.J.; Ip, N.Y.; Radziejewska, E.; Morgenbesser, Cell &S, 663-675, 1991
A;Title: ERK8: a family of protein-serine/threonine kinases that are activated and ty A;Rcterence number: A40033; MUID:91235302; PMID:2032290
A;Status: preliminary
A;Wolecule type: mRNA
A;Residues: 1-358 < MOUN>
Rossomando, A.J.; Martino, P.; Erickson, A.K.; Her, J.H.; Shabanowitz,
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A; Molecule type: mRNA
A; Residues: 1-369 <-HAS.
A; Cross-references: UNIPROT:Q7LZH5; UNIPARC:UPI0000175597
A; Cross-references: UNIPROT:Q7LZH5; UNIPARC:UPI000175597
C; Comment: This enzyme is the key enzyme in the intracellular signal transduction pathwa;
C; Superfamily: kinase-related transforming protein; protein kinase homology
C; Keywords: phosphotransferase
F;32-322/Domain: protein kinase homology <KIN>
                        Z
C;Superfamily: kinase-related transforming protein; protein kinase homology
Keywords: ATP; phosphorotein; phosphoransferase; serine/threonine-specific protein
P;21-311/Domain: protein kinase homology <KIN:
P;29-37/Region: protein kinase ATP-binding motif
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R;Hashimoto, H.; Dokoyama, Y.; Matsuo, Y.; Toyohara, H.; Kohno, M.; Sakaguchi, M.
J. Balchem. 123, 1031-1035, 1998
A;Title: Existence of two isoforms of extracellular signal-regulated kinase in fish.
A;Reference number: JW0052; MUID:98269030; PMID:9603989
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NiAlternate names: CBRK2
NiAlternate names: CBRK2
CiSpecies: Cyprinus carpio (common carp)
CiSpecie: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 KICDFGLARVADPDHDHTGFLTEXVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 NRPIFPGKHYLDQLNHIL--------
                                                                                                                            Query Match

81.4%; Score 1434.5; DB
Best Local Similarity 73.8%; Pred. No. 1.4e-57
Matches 276; Conservative 19; Mismatches 1
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342 KELIFEETARFOPG 355
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C. Accession: A46036
R. Biggs III, W.H.; Zipursky, S.L.
Proc. Natl. Acad. Sci. U.S.A. 89, 6295-6299, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 6295-6299, 1992
A.Title: Primary structure, expression, and signal-dependent tyrosine phosphorylation of A, Reference number: A46036; MUID:92335284; PMID:1378625
A, Recession: A46036
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1.376 & ENIGA
A, Residues: 1.376 & ENIGA
A, Residues: I.376 & ENIGA
A, Note: sequence extracted from NCBI backbone (NCBIN:108684, NCBIP:108685)
C, Genetics:
A, Genetics:
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287 PKALDLIDKMITFNPHKRIEVEAALAHPYLEQYYDPSDEPVAEAPLKFEMELDDLPKETL 346
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MAP Kinase mpk-1 (EC 2.7.1.-) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A56978; T2218
R;Lackner, M.R.; Kornfeld, K.; Miller, L.M.; Horvitz, H.R.; Kim, S.K.
A;Ticle: A MAP kinase homolog, mpk-1, is involved in ras-mediated induction captible number: A36978; MUID:94131270; PMID:8299936
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                            extracellular signal-regulated kinase (EC 2.7.1.-) DMERK-A - fruit fly (Dro
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXVATRWYRAPEIMINSKGYTKSIDIWSVGCILAEMISNRPIFPGKHYLDQLNHI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.4%; Score 1293.5; DB 71.7%; Pred. No. 2.7e-51; tive 22; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251; Conservative
                                                                                                                                        KELIFEETARFOPG
                                                                                                       KELI FQETARFQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 251; Conserva
                                                                                                       317
                                                                                                                                                                   347
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A39754
mitogen-activated protein kinase (EC 2.7.1.-) - African clawed frog
N;Alternate names: M phase MAP kinase
C;Species: Kenpous laevis (African clawed frog)
C;Species: Kenpous laevis (African clawed frog)
C;Species: Xenpous laevis (African clawed frog)
C;Species: Xenpous laevis (African clawed frog)
C;Species: Xenpous laevis (African clawed frog)
C;Date: 07-Feb-1922 #sequence_revision 07-Feb-1922 #text_change 09-Jul-2004
R;Posada, J; Sanghera, J; Pellech, S; Aebersold, R; Cooper, J.A.
Mol. Cell. Biol. 11, 2517-2528, 1991
A;Title: Tyrosine phosphorylation and activation of homologous protein kinases during oc A;Residues: Dreliminary
A;Reference number: A39754
M;Residues: 1736 -POS.
A;Cross references: UNIPARC:UPI0000175592; GB:M60977
R;Gotch, Y; Moriyama, K; Matsuda, S; Okumura, E; Kishimoto, T.; Kawasaki, H.; Suzuki
BMBO J. 10, 2661-2669, 1991
A;Title: Xenpous M phase MAP kinase: isolation of its cDNA and activation by MPF.
A;Residues: Dreliminary
A;Residues: Dreliminary
A;Residues: L-4' G', A', A-28, I', 333-361, A6, 'D', 48, 'V, 50-331, 'F', 333-361, AGT)
A;Cross reference number: S16597
A;Cross references: UNIPARC:UPI00001156A; EMBL:X59813; NID:GA42482.1; PII
C;Superfamily: kinase-related transforming protein; protein kinase homology exila.
F;26-316/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                           241
                                                                            258
                                                                                                                                                                                                                                     293
                                                                                                                                                                                                                                                                                                 259 -ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLK 317
                                                                                                                                                                                                                                                                                                                                      294 KALDLIDKMLTFNPHKRIEVEEALAHPYLEQYYDPTDEPVAEAPFKFDMELDDLFKETLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 VODLMETDLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLLNTTCDL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNAD 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
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                                                                                                                                                                                                                                  234 RPIFFGKHYLDQLNHILGILGSPSQEDLNCIINIKARNYLLSLPLRCKVPWNRLFPNADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                ELIFQETARFOPG 330
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ELIFEETARFQPG 366
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Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                318
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202 YQILRGLKYIHSANVLHRDLKPSNLLLNTTCDLKICDFGLARVTDPQTDHTGFLTBYVAT 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 RWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHIL------, 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ALDLLDRMLTFNPNKRITVEEALAH 283
                                                                                                                                                                                       YQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTBYVAT
                                                                                                                                                                  88 EIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogenicity MAP kinase 1 [imported] - Pyricularia grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 PYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.4%; Score 907; DB 2;
llarity 52.2%; Pred. No. 4.1e-34;
Conservative 47; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
    ; Pred. No. 2.96
33; Mismatches
  70.0%;
    Local Similarity 70.0
nes 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-356 <XUJ>
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       Best Loca
Matches
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A; Residues: 1-376 claC>
A; Cross-references: UNIPROT: P39745; UNIPARC: UPI000002B465; GB:U27124; GB:S68854; NID:gB6
R; Cross-references: UNIPROT: P39745; UNIPARC: UPI000002B465; GB:U27124; GB:S68854; NID:gB6
R; Cross-reference number: Z19519
A; Recension: T2218
A; Recension: T2218
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-376 cWIL>
C; Superfamily: kinase-related transforming protein; protein kinase homology
F; 26-285/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Suppression of activated Let-60 ras protein defines a role of Caenorhabditis el A;Reference number: A36977; MUID:94131269; PMID:8299935 A;Accession: A36977 A;Accession: A36977 A;Equus: preliminary A;Molecule type: mRNA A;Residues: 1-444 <WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: P39745; UNIPARC: UP10000164181; GB: U03879; NID: 9433356; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQILKGLKYIHSANVLHRDLKPSNLLLINTTCDLKICDFGLARVTDPQTDHTGFLTEYVAT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMBTDLYKLLKSQQLSNDHICYFL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTBYVAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ALDLLDRMLTFNPNKRITVEEALAH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VEEVHGQLFEVAPRYVNLSYIGEGAYGWVASALDTITRDRVAIKKISPFEHQTFCQRTLR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A36977
MAP Kinase sur-1 (EC 2.7.1.-) - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C.Accession, A36977
G.Accession, A36977
Genes Dev. 8, 147-159, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 VEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQRTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.1%; Score 1272; DB 2; Length 376; 70.0%; Pred. No. 2.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYLEQYYDPGDEPVCEEPFTLEMEFDDLPKEKLKELIWEE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 238;
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R;Xu, J.R.; Hamer, J.E.
Genes Dev. 10, 2696-2706, 1996
A;Title: MAP Kinase and CAMP signaling regulate infection structure formation and pathoge
A;Reference number: Z25880; MUID:97102671; PMID:8946911
                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:092246; UNIPARC:UPI000006C824; EMBL:U70134; PIDN:AAC49521.2 A;Experimental source: strain Guyll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LALDLLDRMLTFNPNKRITVEEALAHPYLEQYYD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
C;Species: Pyricularia grisea
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51944
                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 39/2; 232/1
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 FDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 YIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVATRWYRAPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
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RESULT 14

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72.1%; Score 1272; DB 2; Length 444;

Query Match

C;Keywords: ATP; phosphotransferase F;94-353/Domain: protein kinase homology <KIN> F;102-110/Region: protein kinase ATP-binding motif

Title: US-10-623-108-2 Perfect score: 1763 Sequence: 1 MAAAAAQGGGGEPRRTEGV...........LKELIFQETARFQPGVLEAP 335

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 2166443 seqg, 705528306 residues Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	Q8nhx0 homo sapien	,C	E	P21708 r mitogen-a		Q7m0h9 cricetulus		Q71zh4 cyprinus ca		_	Q9dgr6 brachydanio	bost	P28482 homo sapien	P63085 mus musculu			Q7z3h5 homo sapien			P26696 xenopus lae	cyprinus	•••		_	brachyda	Q6dfk6 xenopus lae	Q4rv04 tetraodon n				Q4h315 ciona intes
		1																															
SUMMAKIES		ΩI	Q8NHX0 HUMAN	MK03 HUMAN	MK03 MOUSE	MK03_RAT	Q4PIY8 RAT	Q7M0H9_CRIGR	Q8NHX1 HUMAN	Q7LZH4_CYPCA	Q8UWG6 CHICK	Q7ZVK8_BRARE	Q9DGR6_BRARE	MK01 BOVIN	MK01 HUMAN	MK01 MOUSE	MK01_RAT	Q6P023 BRARE	Q7Z3H5 HUMAN	QSNVR1_PONPY	Q7LZH5_CYPCA	MK01 XENLA	Q61811 CYPCA	Q5D061_XENLA	Q4VH14_BRARE	Q7ZW72 BRARE	Q9DGR5_BRARE	Q6DFK6_XENLA	Q4RV04 TETNG	Q4S9M7 TETNG	Q16945_APLCA	Q8IS92_STRPU	Q4H3L5_CIOIN
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		Match Length	335	379	380	380	380	369	357	392	368	392	391	360	360	358	358	369	323	358	369	361	369	361	369	369	369	361	366	358	351	369	350
,	Query	Match	99.7	98.2	94.1	93.9	93.9	95.8	86.4	82.6	82.2	82.2	82.1	82.0	81.9	81.4	81.4	81.3	81.3	81.3	81.3	81.2	81.2	81.1	81.0	80.9	80.8	80.4	80.4	80.1	77.8	77.0	75.2
		Score	1757	1731	1659	1656	1656	1636	1522.5	1455.5	1449	1448.5	1447.5	1445.5	1444.5	1434.5	1434.5	1434	1433	1433	1433	1431	1431	1429	1428	1427	1424	1418	1417	1412	1372	1358	1325
	Result	No.	-	7	e	4	ß	9	7	80	*57	131	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

paralichthy halocynthia		drosophila drosophila				_	anopheles g	podospora a		gibberella
Q8ayi0 Q8mxz5	Q86n95 Q5k4t9	P40417 Q7p159	060rp3	P39745	Q6pmm5	035558	Q7pvr1	Q874z6	09c1e0	Q41883
Q8AYIO PAROL Q8MXZ5_HALRO	Q86N95 MARGL Q5K4T9 9BILA	ERKA DROME 07PLS9 DROME	Q60RP3_CAEBR	SUR1_CAEEL	Q6PMM5_SCHJA	O35558_MOUSE	Q7PVR1_ANOGA	Q874Z6 PODAN	Q9C1E0 NEUCR	Q418S3_GIBZE
00	0 0	4 6	~	-	~	N	~	~	~	7
395 362	372 394	376 376	374	444	351	291	230	353	352	355
74.8	74.0	73.4	72.3	72.1	65.8	64.6	55.1	52.1	52.1	52.1
1318.5	1304.5	1293.5	1275	1272	1159.5	1139	972	919	918	918
32	3.4 3.5	36	38	39	40	41	42	43	44	45

### ALIGNMENTS

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121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                             Olocr-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Extracellular signal-related kinase 1c.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Evarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abbersold D.M., Yung Y., Seger R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX033608; AXKS2330.1; -; mRNA.
HSSP; P28482; 1PME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 AA; 38249 MW; A82027A684BA12E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO170; ERKIERKZMAPK.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKC; 1.
PROSITE; PS01351; MAPK; UNKNOWN 1.
PROSITE; PS0101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROFITE; PSS0101; PROTEIN KINASE DOM; 1.
STEP-binding; Kinase; Nucleotide-binding;
Serine/threonine-protein kinase; Transferase.
                                                                                                    335 AA
                                                                                                    PRT;
                                                                                              QBNHXO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 334; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMR; Q8NHX0; 29-330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Ensembl;
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 MEDINE-Lymph,

XI STGE-Lymph,

XI STGE-LYMPH S. J. Wagner L. M. Derge J.G.,

XI STGE-LYMPH S. J. Wagner L. M. Schuler G.D.,

XI STGE-LYMPH S. J. Wagner L. Max S. I., Wang J., Heileh F.,

XI STGHLIA S. J. J. Warnsina K., Farmer A.A., Rubin G.M., Hong L.,

XI STGH-GENKO L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XI STGH-GENKO L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XI STGH-GENKO L., Marusina R., J. Abramson R.D., Millahy S.J.,

XI STGH-GENKO L., Marusy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XI STGH-GENKO L., Maruy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XI Halon D. K., Muruy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XI Halon D. K., Maruy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XI Halon B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

XI Hakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

XI Schmerch A., Schein J.B., Jones S.J.M., Marra M.A.,

XI Scherzation and initial analysis of more than 15,000 full-length human
121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL 180
                            KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                        240
                                                                                   NRPIFPGKHYLDQLNHILALDLLDRMLTFNPNKRITVERALAHPYLEQYYDPTDEPVAEE 300
                                                                                                   241 NRPIFPGKHYLDQLNHILALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEE 300
                                            Eukaryofa, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92171961; PubMed-1540184;
Owaki H., Makar R., Boulton T.G., Cobb M.H., Geppert T.D.;
"Extracellular signal-regulated kinases in T cells: characterization
of human ERK1 and ERK2 CONSs.";
                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitogen-activated protein kinase 3 (EC 2.7.1.37) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase)
(MAP kinase 1) (MAPK 1) (p44-ERK1) (ERT2) (p44-MAPK) (Microtubule-associated protein 2 kinase).

Name=MAPK3; Synonyms=ERK1, PRKM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Charest D.L., Jirik F., Harder K., Pelech S.L., Mordret G.; "Molecular cloning, expression, and characterization of the human mitogen-activated protein kinase p44erkl."; Mol. Cell. Biol. 13:4679-4690(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 182:1416-1422(1992)
                                                                                                                                                            301 PFIFAMELDDLPKERLKELIFQETARFQPGVLEAP 335
                                                                                                                                           301 PFTFAMELDDLPKERLKELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                                            379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93330262; PubMed=7687743;
                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 14-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 25-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23,
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEOUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Hepatoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                              HUMAN
                                                                                      241
                             181
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"Human immunodeficiency virus type 1 Nef binds directly to LCK and
"Human immunodeficiency virus type 1 Nef binds directly to LCK and
"Human immunodeficiency virus type 1 Nef binds directly to LCK and
"The directivated protein kinase, inhibiting kinase activity.";

"I J. Virol. 70:6701-6708(1996).

"I FUNCTION: Involved in both the initiation and regulation of
melosis, mitosis, and postmitotic functions in differentiated
cells by phosphorylating a number of transcription factors such as
ELK-1. Phosphorylates EIF4EBP1, required for initiation of
translation. Phosphorylates microtubule-associated protein 2
(MAP2) (By similarity).

-!- CAPALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated in

-!- COPACTOR: Magnesium (By similarity).

-!- ENZWHE REGULATION: Activated and tyrosine phosphorylated in
response to insulin and NGFE.

-!- SUBBUNIT: Binds to HIV-1 Nef. This interaction inhibits its kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1770; ERKIERENAPR.

PRINTS; PRO1772; JNKMAPKINASE.

PRODON: PRO0001; Proc. Kinase; 1.

PROSITE; PS01351; MAPK; 1.

PROSITE; PS01351; MAPK; 1.

PROSITE; PS01007; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.

DOMAIN 42 330 Protein kinase.
MEDLINE=92316223; PubMed=1319925; DOI=10.1016/0014-5793(92)80612-K; Gonzalez F.A., Raden D.L., Rigby M.R., Davis R.J.; "Heterogeneous expression of four MAP kinase isoforms in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: Autophosphorylated on threonine and tyrosine residues (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG. GO: 0005524; F:ATP binding; NAS.

GO; GO: 0004707; F:MPP kinase activity; NAS.

GO; GO: 0004707; F:MPP kinase activity; NAS.

GO; GO: 0000648; P:protein amino acid phosphorylation; IDA.

GO; GO: 0000674; P:regulation of cell cycle; NAS.

InterPro; IPR008319; DIVE MAP.

InterPro; IPR00831; NNE MAP.

InterPro; IPR00871; MAP.Kin.

InterPro; IPR00871; Prot. kinase.

InterPro; IPR00871; Ser_thr pkin AS.

InterPro; IPR008299; Ser_thr pkinase.

Prof. Rinase.

Prof. Rinase.

Prof. Rinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53355:DAPK1, NDExp=3; INLACL=EBI-73995, EBI-358616; O75676:RPS6KA4; NDExp=1; INLACL=EBI-73995, EBI-73933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENSG0000102882; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X60188; CAA42744.1; -; mRNA.
EMBL; BC013992; AAH13992.1; -; mRNA.
EMBL; B4490; AAA36142.1; -; mRNA.
EMBL; Z11696; CAA77754.1; -; mRNA.
                                                                                                                                                                                  FEBS Lett. 304:170-178(1992)
                                                                                                                                                                                                                                                                             INTERACTION WITH HIV-1 NEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNC; HGNC:6877; MAPK3.
H-InvDB; HIX0012930; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A48082; A48082.
HSSP; P28482; 1PME.
SMR; P27361; 29-374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reactome; P27361; -. MIM; 601795; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- INTERACTION:
                                                                                                                                                                                                                                                                                                                      PubMed=8794306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity
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us-10-623-108-2.rup

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C STRAIN=FVB/N; ITSSUE=Kidney, and Mammary tumor;

STRAIN=FVB/N; ITSSUE=Kidney, and Mammary tumor;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKALDLIDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAESPFTFAMELDDLPKERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VODLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRPI PPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLPPKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMBLDDLPKERL
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAAAAQGGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                          1 MAAAAAQGGGGGPRRTEGVGPGVPGVPGVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                  Gaps
                        Proton acceptor (By similarity).

ATP (By similarity).

Prosphothreonine (activates the kinase)

Phosphotyrosine (activates the kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MK03_MOUSE STANDARD; PRT; 380 AA.
063844; O61531; O8KOX5; O21YW5;
01-NOV-1997 (Rel. 35, Created)
13-SEP-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitogen-activated protein kinase 3 (EC 2.7.1.37) (Extracellular mitogen-activated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase)
(MAP kinase 1) (MAPK 1) (P44-ERK1) (ERT2) (p44-MAPK) (Microtubule-associated protein 2 kinase) (MMK1).
                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                          Length 379;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                               -> S (in Ref. 1).
E6020CE413EC41F7 CRC64;
ATP (By similarity).
                                                                                                                                                                                                                                      Score 1731; DB 1;
Pred. No. 1.7e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRPIFPGKHYLDQLNHIL-------
                                                                                                                                                                                                                                                                                                  0; Mismatches
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KELIFOETARFOPGVLEAP 335
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                                                                                                                                                                                                                                      98.2%;
                                                                                                                                                                                 43136
                                                                                                                                                                                                                                                                                               Matches 335; Conservative
56
166
71
202
204
174
                                                                                                                                                                           379 AA;
                                                                                                                                                                                                                                                                         Similarity
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NP_BIND
ACT_SITE
BINDING
MOD_RES
MOD_RES
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                                                                                                                                               CONFLICT
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CBA; TISSUB=Bone marrow;
MEDININE=93185941; PubMed=8444355; DOI=10.1016/0378-1119(93)90411-U;
MEDININE=93185941; PubMed=8444355; DOI=10.1016/0378-1119(93)90411-U;
Brainler M.A., Nagorskaya T.V., Visser J.W.M., Belyavsky A.V.;
"Novel CDC2_related protein kinases produced in murine hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUCLEOTIDE SEQUENCE OF 171-205.

MEDLINE=93092802; PLDMed=1459009;

Ershlar M.A., Nagorskaya T.V., Visser J.W.M., Belyavsky A.V.;

Ershlar M.A., Nagorskaya T.V., Visser J.W.M., Belyavsky A.V.;

Ershlar M.A., Nagorskaya T.V., Visser J.W.M., Belyavsky A.V.;

cdc2 family and expressed in murine hematopoietic stem cells.";

Dokl. Akad. Nauk SSR 324:893-897(1922).

1- FUNCTION: Involved in both the initiation and regulation of melosis, mitosis, and postmitotic functions in differentiated cells by phosphorylating a number of transcription factors such such in Phosphorylates EIF4EBP1; required for initiation of translation. Phosphorylates microtubule-associated protein 2 (MAP2) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Crews C.M., Alessandrini A.A., Erikson R.L.;
"Mouse Erk-1 gene product is a serine/threonine protein kinase that
has the potential to product te tyrosine.";
proc. Natl. Acad. Sci. U.S.A. 88:8845-8849(1991).
                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 4-380.
PubMac=8424957; DOI=10.1016/0167-4781(93)90074-N;
Tanner B., Mueckler M.;
"Molecular cloning of a mouse extracellular signal regulated kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de Miguel C., Kligman D., Patel J., Detera-Wadleigh S.D.; "Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse and rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorylation. PTM: Autophosphorylated on threonine and tyrosine residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .!-CTALYTIC ACTIVITY: A7/:
-!-COFALYTIC ACTIVITY: A7/:
-!- COFALYTIC ACTIVITY: ACTIVITY:
-!- COFALYOR: Magnesium (By similarity).
-!- ENZYME REGULATION: Activated by tyrosine and threonine
                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1171:319-320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC013754; AAH13754.1; -; mRNA.
EMBL; BC029712; AAH29712.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91369479; PubMed=1716439;
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pre-B cell;
MEDLINE=92020947; PubMed=1717989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Cell Biol. 10:505-514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 171-209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 77-380.
                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 10-19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells.";
                                                                                                                                                            and mouse
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EMBL; S58470; AAB19973.1; -; mRNA. EMBL; X64605; CAA45889.1; -; mRNA. PIR; S28184; S28184. HSSP; P28482; 1PME.

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RESULT
                                           M GO, GO:0005737; C:cytoplasm; IDA.

R GO, GO:0007707; FiNAP kinase activity; IMP.

R GO, GO:000787; F:protein binding; IPI.

R GO, GO:0004672; F:protein kinase activity; IDA.

R GO, GO:0006468; P:protein kinase activity; IDA.

R GO, GO:0006974; P:response to DNA damage stimulus; IDA.

R GO, GO:0006974; P:response to DNA damage stimulus; IDA.

R GO, GO:0007165; P:signal transduction; TAS.

R GO, GO:0007165; P:signal transduction; TAS.

R InterPro; IPR008349; Erk 1 2 MAPK.

R InterPro; IPR008357; MAP kin.

R InterPro; IPR000257; MAP kin.

R InterPro; IPR000271; Ser Ehr pkin AS.

R RINTS; PR01770; PRNUARENARK.

R RINTS; PR01772; JNKMAPKINASE.

R ROSITE; PS00107; PROTEIN KINASE ATP; 1.

R ROSITE; PS00107; PROTEIN KINASE BOM; 1.

R PROSITE; PS00107; PROTEIN KINASE BOM; 1.
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RPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDS 302
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ATP (By similarity).
ATP (By similarity).
ATP (By similarity).
Phosphothreonine (activates the kinase)
(By similarity).
Phosphotyrosine (activates the kinase)
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Pred. No. 5.4e-96;
1; Mismatches 10; Indels 4
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(By similarity).
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                   Ensembl; ENSMUSG00000063065; Mus musculus.
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Best Local Similarity 85.4%;
Matches 323; Conservative
                                      MGI:1346859; Mapk3
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ACT SITE
BINDING
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MKO3 RAT

AC P21708; Q62686; O9JJ13;

AC P21708; Q62686; O9JJ13;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 13-SEP-2005 (Rel. 26, Last annotation update)

DT 13-SEP-2005 (Rel. 27, Last sequence update)

DE Mitogen-activated protein kinase 3 (EC 2.7.1.37) (Extracellular DE signal-regulated kinase 1) (RFK-1) (Insulin-stimulated MAP2 kinase)

DE MAPR kinase 1) (MAPK 1) (Q44-ERK1) (ERT2) (p44-MAPK) (Microtubule-DE associated protein 2 kinase) (MMXI).

CN Name=Mapk3; Synonyms=Erk1, Prkm3;

CN Rattus norvegicus (Rat).

CO Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CO Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

CO Murcidea; Muridae; Mutinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE OF 7-180.
Maisonpierre F.C., le Beau M.M., Espinosa R. III, Ip N.Y.,
Maisonpierre J. L., la Monte S.M., Squinto S., Furth M.E., Yancopoulos G.D.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=90312137; PubMed=2164259;
Boulton T.G., Yancopoulos G.D., Gregory J.S., Slaughter C., Moomaw C., Hsu J., Cobb M.H.;
Hsu J., Cobb M.H.;
"An insulin-stimulated protein kinase similar to yeast kinases involved in cell cycle control.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 43-64 AND 167-185, AND CHARACTERIZATION.
MEDLINE=91105092; PubMed=1846291;
Boulton T.G., Gregory J.S., Cobb M.H.;
"Purification and properties of extracellular signal-regulated kinase
1, an insulin-stimulated microtubule-associated protein 2 kinase.";
Biochemistry 30:278-286 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=91296777; PubMed=1712480; Seger R., Ahn N.G., Boulton T.G., Yancopoulos G.D., Panayotatos N., Seger R., Ahn N.G., Boulton T.G., Yancopoulos G.D., Fanayotatos N., Radziejewska E., Ericason L., Bratlien R.L., Cobb M.H., Krebs E.G.; "Microtubula-essociated protein 2 kinases, ERK1 and ERK2, undergo autophosphorylation on both tyrosine and threonine residues: implications for their mechanism of activation."; Proc. Natl. Acad. Sci. U.S.A. 88:6142-6146(1991).
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MEDLINE-9136479; PubMed=1716439;
MEDLINE-9136479; PubMed=1716439;
MEDLINE-9136479; PubMed=1716439;
Med Miguel C., Kligman D., Patel J., Detera-Wadleigh S.D.;
"Molecular analysis of microtubule-associated protein-2 kinase CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-93013050; PubMed=1327976; DOI=10.1016/0378-1119(92)90109-3;
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MEDIJINE=20283605, PubMed=1074187, DOI=10.1074/jbc.M910060199;
MEDIJINE 2. Hanoch T., Seger R.;
"ERKIb, a 46-kDa ERK isoform that is differentially regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95025978; PubMed=7939721;
Lin T.-A., Kong X., Haystead T.A.J., Pause A., Belsham G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 14-380, AND PARTIAL PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marquardt B., Stabel S.;
"Sequence of a rat cDNA encoding the ERK1-MAP kinase.";
Gene 120:297-299 (1992).
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DNA Cell Biol. 10:505-514(1991).
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                             translation initiation.";
Science 266:653-656(1994).
-!- FUNCTION: Involved in both the initiation and regulation of melosis, mitosis, and postmitotic functions in differentiated cells by phosphorylating a number of transcription factors such as ELK-1. Phosphorylates BIF48BP1; required for initiation of translation. Phosphorylates microtubule-associated protein 2 (MAP2) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Prot_Kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS01151; MAPK; 1.
PROSITE; PS001107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Alternative splicing; ATP-binding; Cell cycle;
Direct protein sequencing; Kinase; Nuclear protein;
Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                   IsoId=P21708-2; Sequence=VSP 004830; TISSUE SPECIFICITY: Highest levels within the nervous system, expressed in different tissues, mostly in intestine, placenta and
                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: Increased expression during development. PTM: Autophosphorylated on threonine and tyrosine residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase subfamily.
                                                                                                                                               CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. COFACTOR: Magnesium (By similarity).
ENZYME REGULATION: Activated and tyrosine phosphorylated in response to insulin and NGF.
SUBCELLULAR LOCATION: Nuclear (isoform B).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005822; C:cytosol; IDA.

GO; GO:0005825; C:cytosol; IDA.

GO; GO:0004707; F:MAP kinase activity; TAS.

GO; GO:0004707; F:MAP kinase activity; TAS.

GO; GO:00045941; P:positive regulation of kanscription; IEP.

GO; GO:0005486; P:protein amino acid phosphorylation; IEP.

GO; GO:000743; P:protein amino acid phosphorylation; TAS.

R InterPro; IPR008349; Erk 1 2 MAPK.

R InterPro; IPR00831; JMK MAPK.

R InterPro; IPR00831; JMK MAPK.

R InterPro; IPR00831; Ser Lhr pkinase.

R InterPro; IPR00821; Ser Chr pkinase.

R InterPro; IPR00821; Ser Chr pkinase.

R InterPro; IPR00821; Ser Chr pkinase.
   Sonenberg N., Lawrence J.C. Jr.; "PHAS-I as a link between mitogen-activated protein kinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X65198; CAA46318.1; -; mRNA.
EMBL; M61177; AAA63486.1; -; mRNA.
EMBL; M38194; AAA41123.1; -; mRNA.
EMBL; U12008; AAA20009.1; -; mRNA.
EMBL; AF155236; AAF71666.1; -; mRNA.
PIR; JC1451; JC1451.
HSSP; P28482.1 PME.
SMR; P21708; 30-375.
Ensembl; ENSRNOG0000019601; Rattus norvegicus.
                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms-2;
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PRINTS; PR01772; JNKMAPKINASE.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                     44; Gaps
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Proton acceptor (By similarity).
ATP (By similarity).
Phosphothreonine (activates the kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDI.NE=93013050; PubMed=1327976; DOI=10.1016/0378-1119(92)90109-3; Marquardt B., Stabel S.; Sequence of a rat cDNA encoding the ERK1-MAP kinase.";
                                                                             (By similarity). Phosphotyrosine (activates the kinase) (By similarity).
                                                                                                                                              -> EVSRPPAAGRGISVPSVRPVPYCLCPQ (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                               Query Match 93.9%; Score 1656; DB 1; Length 380; Best Local Similarity 85.4%; Pred. No. 8.3e-96; Matches 323; Conservative 1; Mismatches 10; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

93.9%; Score 1656; DB 2; Length 380;
Best Local Similarity 85.4%; Pred. No. 8.3e-96;
Matches 323; Conservative 1; Mismatches 10; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 RPIFPGKHYLDQLWHIL-------
                                                                                                                                                                                                                                                   53785C4ED722723A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA; 42981 MW; 53785C4ED722723A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                        isoform B).
/FTId=VSP 004830.
G -> R (in Ref. 4).
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 ELIFQETARFQPGAPEAP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 ELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                              95 C
42981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4PIY8 RAT PRELIMINARY;
Q4PIY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
       167
72
203
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                                                                                                                                                                                                                              95
380 AA;
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                                                      203
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                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                           SEQUENCE
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Extracellular signal-related kinase 1b.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aebersold D.M., Yung Y., Seger R.;
Submitted (APR-2201) to the EMBL/GenBank/DDBJ
BEDL; AY033607; AAK52329.1; -; mRNA.
HSSP; P28482; IPME.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclectide-binding;
Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                QBNHX1 HUMAN PRELIMINARY;
Q8NHX1;
                                                                                                        Best Local Similarity 85.6
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                 FQPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                    361 FÓPGAPEAP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
NUCLEOTIDE SEQUENCE.
                                                                            369 AA;
                                                                                                                                                                                                                                                                                       LDQLNHIL-
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                                                         NON TER
NON TER
SEQUENCE
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                                      HVRKTRVAIKKISPFEHOTYCORTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIV 121
                                                 QDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLK 181
                                                                                        ICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSN 241
                                                                                                                            183 ICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSN 242
                                                                                                                                                       ----- 258
                                                                                                                                                                         RPIFPGKHYLDÓLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDS 302
                                                                                                                                                                                           -ALDLLDRMLTFNPNKRITVERALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKBRLK 317
                                                                                                                                                                                                     KALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFDMELDDLPKERLK 362
                   62
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            AAAAAPGGGGGEPRGTAGUVPVVPGEVEVVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD
  AAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD
                                                                                                                                                                                                                                                                                                                                                                 Cricetulus griseus (Chinese hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Cricetulus.
                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) ERK1
                                                                                                                                                       RPIPPGKHYLDQLNHIL-------
                                                                                                                                                                                                                                                                                                 369 AA
                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                             ELIFOETARFOPGVLEAP 335
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PRINTS; PR01772; JNKMAPKINASE.
                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                Q7m0H9 CRIGR PRELIMINARY;
Q7m0H9;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||||
241 LDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRAPTLEAMRDVYIVQDLMETDLY
                                                                                                                                                                                                                                                                                                                                                                                              KKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 ADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHY
                                                                                                                                                         11 GGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAI
                                                                                                                                                                                                             1 GGEPRGAAGVGPGVPGEVEVVKGOPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAI
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMR; OBNHXI; 29-344.

Bnsembl; ENSGO000102882; Homo sapiens.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004707; F:MP binding; IEA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004678; F:Protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPRO08349; Erk 1.2 MAPK.

InterPro; IPRO08351; MAPKin.

InterPro; IPRO00719; Prof kinase.

InterPro; IPRO02290; Ser_thr_pkinase.
                                                                                                     44;
                                                      369;
                                                 92.8%; Score 1636; DB 2; Length 3
85.6%; Pred. No. 1.4e-94;
ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases.
42126 MW; OBBSFCAAC690B4FF CRC64;
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62 16 196

122

256 242

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257 PIFPGKHYLDÖLNHILGILGSPTQDDLNCIINMKARNYLQALPQKPKIPWNKLFPKADNK 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALDLIDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AAVAVGGANG-----AAGP-KPG-LESVKGQNFDVGPRYTDLQYIGEGAYGMVCSAFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 CDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDMWSVGCILAEMLSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 CDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Pineal gland;
Kasahara T., Higashi C., Okano T., Fukada Y.;
Kasahara T., Higashi C., Okano T., Fukada Y.;
Bubmitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AY033635; ARK56503.1; -; MRNA.
HSSP; P28482; IPME.
SWR, O8UWG6; 24-367.
Ensembl; ENSGALG0000001501; Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 392;
GO; GO:0006468; P:protein amino acid phosphorylation; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                         82.6%; Score 1455.5; DB 2; Length
77.3%; Pred. No. 3.1e-83;
tive 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                     392 AA; 44133 MW; 02EE90132E5C347B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 AA
                                                                                                                                                                                                                                                                                                                                                              Serine/threonine-protein kinase; Transferase.
SEQUENCE 392 AA; 44133 MW; 02EE90132E5C34
                    InterPro; IPR00349; Erk 1 2 MAPK.
InterPro; IPR003527; MAP kin.
InterPro; IPR000719; Proc kinase.
InterPro; IPR000719; Proc kinase.
Pfam; PF00069; Pkinase; I.
PRINTS; PR0177; ERKIERKISMAPK.
PROSITE; PS00107; PROFEIN KINASE ATP; I.
PROSITE; PS00107; PROFEIN KINASE DOM; I.
PROSITE; PS00108; PROFEIN KINASE DOM; I.
PROSITE; PS00108; PROFEIN KINASE DOM; I.
PROSITE; PS00108; PROFEIN KINASE ST; I.
PROSITE; PS00108; PROFEIN KINASE ST; I.
PROSITE; PS00108; PROFEIN KINASE ST; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular signal-regulated kinase 2. Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBUWG6_CHICK
ID QBUWG6_CHICK PRELIMINARY;
AC QBUWG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286; Conservative
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LIYEETARFO 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAAAAAQGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTLEMA CYPCA PRELIMINARY; PRT; 392 AA.
O7LZH4;
O1-MAR-2004 (TEMBLrel. 26, Created)
O1-MAR-2004 (TEMBLrel. 26, Last sequence update)
O1-PRB-2005 (TEMBLrel. 29, Last annotation update)
Extracellular signal-regulated kinase (EC 2.7.-.-) 1 (Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -: SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-: SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB006038; BAD23842.1; -; mRNA.
PIR; VM0622; 0W0052.
SMR; Q7LZH4; 39-386.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:000654; F:ATP binding; IEA.
GO; GO:0004670; F:MPP kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                          DB 2; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Existence of two isoforms of extracellular signal-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hashimoto H., Yokoyama Y., Matsuo Y., Toyohara H., Kohno M. Sakaguchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKALDLIDRMLTFNPNKRITVEEALAHPYLEQYYDPTDE-VGQSP 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEP 301
                                                                                                                                                                                                                                                                                                                                    Query Match 86.4%; Score 1522.5; DB 2; Length Best Local Similarity 85.8%; Pred. No. 1.8e-87; Matches 296; Conservative 1; Mismatches 3; Indels
                               PRINTS; PRO1770; ERKIERKZWAPK.
PRINTS; PRO1770; ERKIERKZWAPK.
PRODUCTS; PRO1772; UNKWAPKINASE.
PRODUCTS; PRO1721; PROC. I.
SWART; SM00220; S. TKC; I.
PROSITE; PS01351; PROTEIN KINNSE ATP; 1.
PROSITE; PS50011; PROTEIN KINNSE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-Binding;
Serine/threonine-protein kinase; Transferase.
SEQUENCE 357 AA; 40062 MW; 58C92773983ADA79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal regulated protein kinase 1)
Name=CERK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Ovary;
MEDLINE=98269030; PubMed=9603989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 123:1031-1035(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Kauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rapleton M., Soares M.B., Bonaldo M.F., Carnhord D.,

RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carnhord P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carnhord P., Prange C.,

RA Brownstein M.J., Widin T.B., Tochiyuki S., Carnhord P., Mullahy S.J.,

Rabas S.A., McEwan P.J., McKernan R.J., Marke J.J., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

R. Halton B.K., McKernan M., Madan A., Rodrigues S., Sanchez A.,

R. Mihting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

R. Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodriguez A. G., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A. G., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

R. Rodriguez A. G., Grimwood J., Schwutz J., Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R SPRIN; DUSDE-GENE-040121-1; mapk3.

R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006704; F:MAP kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR008349; Erk 12 MAPK.
InterPro; IPR008351; JMV MĀPK.
InterPro; IPR008357; MAP kin.
R InterPro; IPR008271; Ser Lhr pkinase.
R InterPro; IPR008271; Ser Lhr pkinase.
R InterPro; IPR008290; Ser thr pkinase.
R PRINTS; PR01770; ERKIERKAMAPK.
R PRINTS; PR01772; JMKMAPKINASE.
R PRODOM; PR000001; Prot kinase; 1.
R PROSITE; PS00107; PROTEIN KINASE APP; 1.
R PROSITE; PS00107; PROTEIN KINASE APP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

82.2%; Score 1448.5; DB 2; Length 392;
Best Local Similarity 76.5%; Pred. No. 8.4e-83;
Matches 283; Conservative 14; Mismatches 28; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krens S.F.G., Snaar-Jagalska B.E., Spaink H.P.;
"Zebrafish ERK1 and ERK2.";
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC045505, AA445505.1;
EMBL; BC0457073; AA445505.1;
EMBL; BC06401; AA466401.1;
EMBL; BC66401; AAY52219;
EMBL; BC66401; AAY57804.1;
EMBL; BC848; 1PWE.
SNR; QZXV8, 41-386.
ZFIN; ZDB-GENE-040121-1; mapk3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44099 MW; C184681E448E5BBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN=AB; TISSUE=Whole body;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOFIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Tuebingen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinase.
SEQUENCE
                DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VODLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 KICDFGLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRPIFPGKHYLDQLNHIL----- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 PKALDLIDKMLTFNPHKRIEVEQALAHPYLEQYYDPSDEPVAEAPFKFDMELDDLPKEKL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAAAAAQGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VAGAAAAGGSAG------AGGPEMVRGQVFDVGPRYTNLSYIGEGAYGMVCSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
   R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004707; F:MAP kinase activity; IEA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

R InterPro; IPR008349; Erk i 2 MAPK.

InterPro; IPR008349; Erk i 2 MAPK.

R InterPro; IPR000357; MAP Kin.

R InterPro; IPR0003590; Ser thr pkin AS.

InterPro; IPR000390; Ser thr pkin AS.

InterPro; IPR000390; Ser thr pkin AS.

R Pfam; PF00069; PK1nase; I.

R PR0MT; SM0020; STKC; I.

R PROSTTE; PS0113; PROTEIN KINASE ATP; I.

R PROSTTE; PS0111; PROTEIN KINASE DOM; I.

R PROSTTE; PS0111; PROTEIN KINASE DOM; I.

R PROSTTE; PS0111; PROTEIN KINASE DOM; I.

R PROSTTE; PS0111; PROTEIN KINASE ST; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Mitogen-activated protein kinase 3 (Extracellular signal-regulated kinase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
NUCLECTIDE SEQUENCE.
STRAIN-AB; TISSUE-Embryo, and Whole body;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
82.2%; Score 1449; DB 2; Length 36
Best Local Similarity 74.6%; Pred. No. 7.3e-83;
Matches 279; Conservative 18; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 KELIPEETARFOPG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7zvke_brare preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232
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AC 072VK
AC 01-JU
DT 01-JU
DT 13-SE
DE Mitog
DE Mitog
DE Name=
GN Name=

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                                                                      122
                                                                                         | DIMETDLYKLIKSQQLSNDHICYFLYQIIRGLKYIHSANVLHRDLKPSNLLINTTCDLKI 182
                                                                                                                                                                                                                                                                                                                                                                        ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEBPFTFAMELDDLPKERLKE 318
62
                 SSAAGPGGAVAPGGPSGAAGSKPG-LESVKGQNFDVGPRYTDLQYIGEGAYGWVCSAFDN 76
                                                                                                                                                                 CDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNR
                                                                                                                                                                                                                                                                                                                            CDFGLARIADPEHDHTGFLTEYVATRWYRAPBIMLNSKGYTKSIDIWSVGCILAEMLSNR
 AAAAQGGGGGEPRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQY1GEGAYGMVSSAYDH
                                                                      VRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLBAMRDVYIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCSI TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hrano T. Priji M.;

Hirano T. Priji M.;

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB030902; BAB11812.1; -; mRNA.

EMBL; AB030902; BAB11812.1; -; mRNA.

BRSP; P28482; 1PME.

SNR; Q9DCR6; 40-385.

SNR; Q9DCR6; 40-385.

SRR; Q9DCR6; 40-385.

SRC; 41-385.

                                                                                                                                                                                                                                                                                                  PIFPGKHYLDQLNHIL--------
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Q9DGR6 BRARB PRELIMINARY;
Q9DGR6;
01-MAR-2001 (TYEMBLY) 16, C:
01-MAR-2001 (TYEMBLY) 16, Li
01-MAR-2004 (TYEMBLY) 26, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIFQETARFQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIFEETARFQ 386
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                                                                                                           77
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                      63 VRKTRVALKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQ 122
                                                                                                                                                                                          75
                                                                                                                                                                   196 CDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 ALDLLDRMLTFNPIKRINVEQALAHPYLEQYYDPSDEPVAEEPFTFNMELDDLPKEKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- COFACTOR: Magnesium (By similarity).
-!- ENTYME REGULATION: Activated by phosphorylation on tyrosine and threonine in response to insulin and NGF.
-!- PTM: Autophosphorylated on threonine and tyrosine residues, which correlates with a slow and low level of autoactivation (By
                                                                                                                                                                                                                                                                                                                                                                                     DLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKI
                                                                                                                                                                                                                                                                                                                                                                                                                         CDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDLEDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKE
                                                                                                                                 3 AAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
13-SEP-2005 (Rel. 48, Last amontation update)
Mitogen-activated protein kinase 10 (ERK-2) (Mitogen-activated protein kinase 2) (MAPK kinase 2) (MAPK 3) (MAPK 2) (MAPK 3) (
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Phosphorylates microtubule-associated protein 2 (MAP2) Myelin basic protein (MBP), and Elk-1; may promote entry in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
TISSUB-Advenal medulla;
Ely Com, Cox M.E., Her J., Parsons S.J.;
Cloning and sequencing of ERK2 from a bovine adrenal medulla CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity). SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
                                                                     45,
   Length 391;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
      5
      DB
82.1%; Score 1447.5; DB 76.5%; Pred. No. 9.6e-83; ive 14; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIFPGKHYLDQLNHIL-
         Query Match
Best Local Similarity 76.5
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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LIFEETARFQ 385
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removed.
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                                                                                                                                                                                                                                                                                                                                                                                DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                                                                                                          44 DIVVNKVRVAIKKISPFEHQTYCQRTLRBIKILLRFRHENIIGINDIIRAPTIEQMKDVYI 103
                                                                                                                                                                                                                                                                                                                                                                                                                     VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                     1 MADADADAGGG------PEWVRGQVFDVGPRYTNLSYIGEGAYGMVCSAY 43
                                                                                                            PRINTS; PRO1770; ERKLERKZWAPK.
ProDom; PRO00001; Prot kinase; 1.
SMART; SM00220; STKC; 1.
PROSITE; PS0131; MAPK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS01018; PROTEIN KINASE ST; 1.
SROSITE; PS011 cycle; Kinase; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                           1 MAAAAAQGGGGGBPRRTEGVGPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                               Phosphothreonine (activates the kinase) (By similarity). Phosphotyrosine (activates the kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
13-SEP-2005 (Rel. 48, Last amnotation update)
Mitogen-activated protein kinase 1 (EC 2.7.1.37) (Extracellular
                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                        DB 1; Length 360;
                                                                                                                                                                                                                             Proton acceptor (By similarity). ATP (By similarity).
                                                                                                                                                                                                                                                                                                                        17; Indels
                                                                                                                                                                                                                                                                            (By similarity).
E85D0B2A4E9549DE CRC64;
                                                                                                                                                                                                 Protein kinase.
ATP (By similarity).
Poly-Ala.
                                                                                                                                                                                                                                                                                                      82.0%; Score 1445.5; DB .74.6%; Pred. No. 1.2e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRPIFPGKHYLDQLNHIL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AA
                                                                                                                                                                                                                                                                                                                         17; Mismatches
                                HSSP; P28482; IPME.
SMR; P46196; 16-359.
InterPro; IPR008349; Brk_1_2_MAPK.
InterPro; IPR000319; Prot_kinase.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_Lhr_pKin_AS.
InterPro; IPR002290; Ser_Lhr_pKin_as.
Pfam; PP00069; Pkinase; I.
                EMBL; Z14089; CAA78467.1; -; mRNA PIR; S25011; S25011.
                                                                                                                                                                                                                                                                                    360 AA; 41376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 KELIFQETARFQPG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279; Conservative
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185
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185
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P28482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344
                                                                                                                                                                                                             NP BIND
COMPBIAS
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BINDING
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                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                        Query Match
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 removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
MK01_HUMAN
ID MK01_HT
AC P28462;
DT 01-DEC:
DT 01-DEC:
DT 13-SEP.
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Matches
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RADILNE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeperg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prenge C.,
RA Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prenge C.,
RA Browstein M.J., Wodin T.B., Toobhlyuki S., Carninci P., Prenge C.,
RA Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92171961; PubMed=1540184; Cobb M.H., Geppert T.D.; Cwaki H., Makar R., Boulton T.G., Cobb M.H., Geppert T.D.; Extracellular signal-regulated kinases in T cells: characterization of human ERK1 and ERK2 COMAs."; Eiochem. Biophys. Res. Commun. 182:1416-1422(1992).
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"Human immunodeficiency virus type 1 Nef binds directly to LCK and
mitogen-activated protein kinase, inhibiting kinase activity.";
mytogen-activated protein kinase, inhibiting kinase activity.";
J. Virol. 70:6701-6708(1986).
-i. FUNCTION: Phosphorylates microtubule-associated protein 2 (MAP2)
(ERK-2) (Mitogen-activated protein kinase (p42-MAPK) (ERT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDILINE-29216223; Publed=1319925; DOI=10.1016/0014-5793(92)80612-K;
GONZAIEZ F.A., Raden D.L., Rigby M.R., Davis R.J.;
"Heterogeneous expression of four MAP kinase isoforms in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myelin basic protein (MBP), and Blk-1; may promote entry in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Belongs to the Ser/Thr protein kinase family. MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                   Name=MAPK1; Synonyms=ERK2, PRKM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 304:170-178(1992).
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             signal-regulated kinase 2)
2) (MAP kinase 2) (MAPK 2)
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                                                                                                                                                 Homo sapiens (Human)
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Eukarmalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
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P63085; P27703;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 24, Last sequence update)
13-SEBP-2005 (Rel. 48, Last annotation update)
2) (MAP kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)
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Best Local Similarity 74.34
Matches 278; Conservative
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R GCRP; P28482; --.

R HANC; BANC: 6871; MARKI.

H-INUDB; HIX0016281; --.

R GO; GO:0006935; P:Chemotaxis; TAS.

R GO; GO:0006935; P:Chemotaxis; TAS.

R GO; GO:0007165; P:SMP kinase activity; TAS.

R GO; GO:0007165; P:SMP kinase.

R InterPro; IPR008349; Erk 1.2 MAPK.

R InterPro; IPR00837; MAP kin.

R InterPro; IPR00827; Ser thr. pkin.

R InterPro; IPR00827; Ser thr. pkin.

R RNOSTE; PR01770; ERKIERKAMAPK.

R RNOSTE; PR01170; ERKIERKAMAPK.

R RNOSTE; PS00107; PROTEIN KINASE ATP; 1.

R RNOSTE; PS00108; PROTEIN KINASE ATP; 1.

R RNOSTE; PROTEIN KINASE ATP; 1.

R RNOSTE; PROTEIN KINASE ATP; 
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ATP (By similarity).
Phosphothreonine (activates the kinase)
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Phosphotyrosine (activates the kinase) (By similarity).
R -> Q (in Ref. 2).
                 EMBL; M84489; AAA58459.1; -; mRNA.
EMBL; Z11694; CAA77755.1; -; mRNA.
EMBL; ELI695; CAA77753.1; ALT_INIT; mRNA.
EMBL; BC017832; AAH17832.1; -; mENA.
PIR; JQ1400; JQ1400.
PDB; IPME; X-ray; @=1-360.
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MEDLINE=229825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=229825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. E., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Araba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunzatane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Youdhan J.W., Shevchenko Y., Bouffard G.G., Malkedley R.W., Touchman J.W., Green E.D., Dickson M.C., Abrack R.W., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., R. Hannan M.A., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. Hannan J., More C., Grimwood J., Smailus D.E., McGeneration and initial analysis of more than 15,000 full-length human
                                                                                            Brehler M.A., Nagorakaya T.V., Visser J.W.M., Belyavsky A.V.;
"Novel CDC2-related protein kinases produced in murine hematopoletic
              MEDLINE=91305126; PubMed=1649458;
Her J.-H., Wu J.-S., Rall T.B., Sturgill T.W., Weber M.J.;
"Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 151-189.
STRAIN=CBA; TISSUE=Bone marrow;
MEDLINE=93185941; PubMed=8444355; DOI=10.1016/0378-1119(93)90411-U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                Nucleic Acids Res. 19:3743-3743(1991).
STRAIN-Swiss, TISSUE-Fibroblast
                                                                    tyrosine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 420:563-573 (2002)
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   . RE REPRESENTE DE LA PRESENTA DE L
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PHOSPHORYLATION SITES THR-183 AND TYR-185, AND PARTIAL PROTEIN

Gene 124:305-306(1993).

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Payme D.M., Rossomando A.J., Martino P., Brickson A.K., Her J.-H.,
Shabanowitz J., Hunt D.F., Weber M.J., Sturgill T.W.;
Indentification of the regulatory phosphorylation sites in
pp42/mitogen-activated protein kinase (MAP kinase).";
EMBO J. 10.885-892(1991).
I. PHOKION: Involved in both the initiation and regulation of
melosis, mitosis, and postmitotic functions in differentiated
cells by phosphorylating a number of transcription factors such as
ELK-I. Phosphorylates microtubule-associated protein 2
(MAP2) (By similarity).
C. I. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorotein.
C. CORACTOR: Magnesium (By similarity).
C. I. ENZYME REGULATION: Activated by phosphorylations and
C. Threonine in response to insulin and NGF. Both phosphorylations
are required for activity (By similarity).
C. I. TISSUE SPECIFICITY: Widely expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: Autophosphorylated on threonine and tyrosine residues, which correlates with a slow and low level of autoactivation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01351; MAPK; 1.
PROSITE; PS0107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS01011; PROTEIN KINASE_ST; 1.
PROSITE; PS01016; PROTEIN KINASE_ST; 1.
ATP-binding; Cell cycle; Direct protein sequencing; Kinase;
Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
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37 ATP (By similarity).

7 Poly-Ala.

147 By similarity.
52 ATP (By similarity).
183 Phosphotyrosine (activates the kinase).
185 Phosphotyrosine (activates the kinase).
186 41276 MW; 3BBCP22471EDBAOB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
kinase subfamily.
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R GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0005737; C:cytoplasm; IDA.

R GO; GO:0001784; F:phosphotyrosine binding; IMP.

R GO; GO:0001784; F:phosphotyrosine binding; IPI.

R GO; GO:000165; F:protein binding; IPI.

R GO; GO:000165; P:protein binding; IDA.

R GO; GO:00006672; F:protein binding; IDA.

R GO; GO:00006463; P:protein amino acid phosphorylation; IDA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IDA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IDA.

R GO; GO:0006974; P:response to DNA damage stimulus; IDA.

R GO; GO:0007655; P:signal transduction; TAS.

R InterPro; IPR008349; Erk 1.2 MAPK.

R InterPro; IPR008349; Erk 1.2 MAPK.

R InterPro; IPR008271; SAR ITA.

R InterPro; PR008271; SAR ITAREXEMAPK.
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EMBL, AK035386; BAC29053.1; -; mRNA.
EMBL, AK048127; BAC33251.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AKO87925; BAC40044.1; -; mRNA.
EMBL; BC058258; AAH58258.1; -; mRNA.
EMBL; D10939; BAA01733.1; -; mRNA.
PIR; S16444; S16444.
SWR; P63085; 14-357.
                          MEDLINE=91184134; PubMed=1849075;
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AUTOPHOSPHORYLATION
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"BERRs: a family of protein-serine/threonine kinases that are activated
and tyrosine phosphorylated in response to insulin and NGF.";
Cell 65:663-675(1991).
                                                                                                                                                                                             VQDLMETDLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLLNTTCDL
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                                                                                                1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P63086; P27703; 01-40G-1992 (Rel. 23, Created) 01-A0G-1992 (Rel. 23, Last sequence update) 13-SEP-2005 (Rel. 24, Last annotation update) 13-SEP-2005 (Rel. 24, Last annotation update) Mitogen-activated protein kinase 1 (EC 2.7.1.37) (Extracellular signal-regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (Rex. 2) (MAP kinase 2) (MAP (2) (M42-MAPK) (ERTI).
                                                          Gaps
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MEDLINE=97442349; PubMed=9298898; DOL=10.1016/S0092-8674(00)80351-7;
Canagarajah B.J., Khokhlatchev A., Cobb M.H., Goldsmith E.J.;
Activation mechanism of the MAP kinase ERX2 by dual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague Dawley; TISSUE=Brain; MEDLINE=91235302; PubMed=2032290; DOI=10.1016/0092-8674(91)90098-J; Boulton T.G., Nye S.H., Robbins D.J., Ip N.Y., Radziejewska E., Morgenbesser S.D., DePinho R.A., Panayotatos N., Cobb M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)

**MEDLINES44150699; PubMed=8107865; DOI=10.1038/36770440;

Zhang F., Strand A., Robbins D., Cobb M.H., Goldsmith B.J.;

"Atomic structure of the MAP kinase ERK2 at 2.3-A resolution.";
                                                        63;
                      Length
                                                        16; Indels
                      DB 1;
                    ; Score 1434.5; DB
; Pred. No. 5.7e-82;
19; Mismatches 16
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                      81.4%;
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Cell 90:859-869(1997).
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                                    Similarity
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DEVELOPMENTAL STAGE: Increased expression during development.
-!- PTM: Autophosphorylated on threonine and tyrosine residues, which correlates with a slow and low level of autoactivation.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 266:653-656(1994).
-1- FUNCTION: Involved in both the initiation and regulation of malosis, mitosis, and postmitotic functions in differentiated cells by phosphorylating a number of transcription factors such ELK-1. Phosphorylates EIF4EBE1; required for initiation of translation. Phosphorylates microtubule-associated protein 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. COFACTOR: Magnesium (By similarity).

ENZYME REGILATION: Activated by phosphorylation on tyrosine and threonine in response to insulin and NGF. Both phosphorylations are required for activity.

TISSUE SPECIFICITY: Highest levels within the nervous system, expressed in different tissues, mostly in muscle, thymus and
MEDLINE 91296777; PubMed=1712480; Seger R., Ahn N.G., Boulton T.G., Yancopoulos G.D., Panayotatos N., Seger R., Ahn N.G., Boulton T.G., Yancopoulos G.D., Fareba E.G., Madziejewska E., Ericsson L., Bratlien R.L., Cobb M.H., Krebs E.G.; Microtubule-associated protein 2 kinases, ERK1 and ERK2, undergo autophosphorylation on both tyroshie and threonine residues: implications for their mechanism of activation.; proc. Natl. Acad. Sci. U.S.A. 88:6142-6146(1991).
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
3D-structure; ATP-binding; Cell Cycle; Kinase; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION OF EIF4EBP1.
MEDLINE=95025978; PubMed=7939721;
Lin T.-A., Kong X., Haystead T.A.J., Pause A., Belsham G.J.,
Sonenberg N., Lawrence J.C. Jr.;
"PHAS-I as a link between mitogen-activated protein kinase and
translation initiation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein kinase.
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InterPro; IPR003527; MAP kin.
InterPro; IPR000719; Proc kinase.
InterPro; IPR008271; Ser Ehr pkin AS.
Pfam; PF00069; Pkinase; I
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PDB; IERK; X-ray; @=1-358.
PDB; IGOL; X-ray; @=1-358.
PDB; ZERK; X-ray; @=1-358.
PDB; 3ERK; X-ray; @=1-358.
PDB; 4ERK; X-ray; @=1-358.
SMR; P63086; 14-357.
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Phosphotyrosine (activates the kinase) (By similarity).
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VQDLMETDLYKLLKSQQLSNDHICYFLYQLLRGLKYIHSANVLHRDLKPSNLLINTTCDL 180

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        181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSYGCILAEMLS 240

        Db
        162 KICDFGLARVADPHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSYGCILAEMLS 221

        Qy
        241 NRPIFPGKHYLDQLAHIL

        222 NRPIFPGKHYLDQLAHILGILGSPSQEDLACIINLKARNYLLSLPHKONYPWNRLFPNAD 281

        Qy
        259 --ALDLLDRMLTENPURRITYBEALAHPYLEQYYDPTDEPVAEEPFFAWELDDLPKERL 316

        Db
        282 SKALDLLKWLTFNPHKRIEVEQALAHPYLEQYYDPSDEPTFAWELDDLPKERL 316

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        282 SKALDLLKWLTFNPHKRIEVEQALAHPYLEQYYDPSDEPTABAPFKFDMELDDLPKERL 341

        Qy
        317 KELIFQFGRARFQPG 330

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        342 KELIFEETARFQPG 355
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317 KELIFQETARFQPGVLEAP 335
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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3: /cgn2 6/ptcdata/1/iaa/H_COMB.pep:*
4: /cgn2 6/ptcdata/1/iaa/RE_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 4, Sequence 4, Sequence 4, Sequence 4, Sequence 12, Sequence 12, Sequence 12, Sequence 34, Sequence 34, Sequence 2, Sequence 2, Sequence 2, Sequence 8, Sequence 8, Sequence 8, Sequence 16, Se		KINASES	Length 379; ; Indels 44; Gaps	GPRYTQLQYIGEGAYGMVSSP 	NVIGIRDILRASTLEAMRDVY 	SANVLHRDLKPSNLLINTTCE	EIMLNSKGYTKSIDIWSVGCILAEML 	NYLQSLPSKTKVAWAKLFPKS	EALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 	DC VALLE LATER CONTRACTOR
1 US-08-458-887-4 2 US-08-932-7878-4 2 US-08-932-012C-4 2 US-08-88-818C-4 2 US-08-176-620-12 1 US-08-176-620-12 1 US-08-461-955-12 1 US-09-457-0408-4 2 US-09-457-0408-3 2 US-09-417-197-41 2 US-09-417-197-59 2 US-09-457-0408-3 2 US-09-642-749-2 1 US-08-457-0408-3 2 US-09-642-749-2 1 US-08-461-985-8 1 US-08-461-985-8 2 US-08-932-7878-16	ALIGNMENTS	1 California 1 California 2, And PREDICTED LEARNING-INDUCEI 1/411,628 1/102,906 18ion 4.0	<pre>k; Score 1731; DB 2; k; Pred. No. 1.2e-173 0; Mismatches 0</pre>	maaaaaqgggggebritgvgpgvpgevemvkgqppdvgbrytqloyigegaygmvssa` 	DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHBNVIGIRDILRASTLEAMRDVY 	ODLMETDLYKLIKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 	HTGFLTBYVATRWYRAP                 HTGFLTBYVATRWYRAP	GKHYLDQLNHILLGKHYLDQLNHILLGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKS	EALAHPYLE           EALAHPYLE	SKALDLILDKALI FNYNAKI I VEBALMUR I LEQI I LETI D
81.5 81.5 81.5 81.5 81.4 81.4 81.4 81.4 81.4 81.4 81.4 81.4		tion US ty of S cDNA, SEQUEN 61-707 NUMBER: 1999- NUMBER: 1998- S: 1998- S: 16 or Wind	similarity 88.4 ³ 5; Conservative	maaaaaggggggeprr 	DHVRKTRVAIKKISPF                DHVRKTRVAIKKISPF	VQDLMETDLYKLLKSQ 	KICDFGLARIADPEHD	NRPI FPGKHYLDQLNHIL               NRPI FPGKHYLDQLNHIL	ALDLLDRMLTFNPNKRITVE	SKADDDDDRMD1FAF
28 29 30 31 32 1436 33 14376 34 143376 37 143376 37 143376 37 143376 37 143376 37 143376 37 143376 37 143376 37 143376 37 143376 47 47 47 47 47 47 47 47 47 47		RESULT 1 US-09-411-628-14 Sequence 14, Applica Patent No. 6428994 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE REFERENCE: 137 CURRENT APPLICATION: CURRENT APPLICATION: FILE REFERENCE: 137 CURRENT FILING DATE BARLIER APPLICATION: CURRENT FILING DATE BARLIER PILING DATE BARLIER PILING DATE SEALIER APPLICATION SOFTWARE: FastSEQ f SEQ ID NO 14 LENGTH: 379 TYPE: PRT CREANISM: Rattus n US-09-411-628-14	Query Match Best Local S Matches 335	Oy 1 Db 1	Oy 61 Db 61	Qy 121 Db 121	Oy 181 Db 181	Oy 241 Db 241	Qy 259	<b>n</b>

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Patent No. 6753314
GENERAL INPORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 1596-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 44;
                                                                                                   USCILLIA APPLICATION US/10174794

| Sequence 14, Application US/10174794
| Patent No. 6664086
| GENERAL INFORMATION:
| APPLICANT: University of Southern California TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES FILE REFERENCE: 13761-707
| CURRENT APPLICATION NUMBER: US/10/174,794
| CURRENT FILING DATE: 1999-10-01 |
| PRIOR APPLICATION NUMBER: US 60/102,906 |
| PRIOR APPLICATION NUMBER: US 60/102,906 |
| PRIOR SEQ ID NATE: 1999-10-01 |
| PRIOR SEQ ID NASE: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.2%; Score 1731; DB 2; Best Local Similarity 88.4%; Pred. No. 1.2e-173; Matches 335; Conservative 0; Mismatches 0;
361 KELIFQETARFQPGVLEAP 379
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US-09-538-092-1021
                                                                         RESULT 2
US-10-174-794-14
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LENGTH: 379
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APPLICANT: Su, Michael Shin-San
APPLICANT: Wilson, Keith Phillip
APPLICANT: Germann, Ureula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
TITLE OF INVENTION: Serine/Thereonine Kinases and Tyrosine Kinase
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                     Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                     ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P27361
US-09-538-092-1021
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ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
                                                                                                                                                                                                                                                                                                                                                  Query Match 98.2%; Score 1731; DB 2; Best Local Similarity 88.4%; Pred. No. 1.2e-173; Matches 335; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPALSeqFormatter Version 0.9
SEQ ID NO 1021
LENGTH: 379
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ORGANISM: Homo sapiens
FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/642,749
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88.1%; Pred. No. 5.1e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 NRPIFPGKHYLDQLNHIL--------
                                                                                                                                                                             NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMPUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                       FILING DATE: 18-Aug-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-417-197-39; Sequence 39, Application US/09417197; Sequence 39, Application US/09417197; Patent No. 6518021; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           LENGTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELIFQETARFQPGVLEAP 335
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Matches 334; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MAAAAAQGGGGGBPRRTEGVGPGVPGEVENVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods For Designing Inhibitors of
Serine/Thereonine Kinases and Tyrosine Kinase
                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAAAAQGGGGEPRRTEGVGPGVPGVERVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                             Length 379;
                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                             Query Match
97.8%; Score 1725; DB 2;
Best Local Similarity 88.1%; Pred. No. 5.1e-173;
Matches 334; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09642749
Patent No. 6849716
GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-San Fox, Ted
Wilson, Keith Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F:
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-025-580-25
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                                                                                                                                                                                                                                                           TOPOLOGY: linear
       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-642-749-25
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APPLICANT: OLITICATION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: On A Cellular Response FITLE OF INVENTION: On A Cellular Response FILE REFERENCE: 3759-0110P CURRENT APPLICATION NUMBER: US/09/417,197 CURRENT FILING DATE: 1999-10-07 NUMBER OF SEQ ID NOS: 143 SOFTWARE: Patentin version 3.0 SEQ ID NO 39
                                                                                                                                                                                                                                                                      240
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                                                                                                                                                                         9
                                                                                                                                                 1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                  1 MAAAAAQGGGGGPPRRTEGVGPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAY
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Length 379;
                                                          Indels
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FEATURE:
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                                                                                                                                                                                                                                                                                            VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258
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                                                                                                                                                                                                                                                                                                                                                                                                                                    433 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMINSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
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                                                                                                                                                                                                1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                              44; Gaps
                                                                                                                            Length 631;
                                                                                                                      Query Match
97.8%; Score 1725; DB 2; Length 63:
Best Local Similarity 88.1%; Pred. No. 1.1e-172;
Matches 334; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,277A
FILING DATE: 27-MAR-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 320577-1995
FILING DATE: 08-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 305456-1995
FILING DATE: 24-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-08-622-277A-8
US-08-622-277A
Sequence 8, Application US/08622277A
Patent No. 6001580
GENERAL INFORMATION:
APPLICANT: Tani, Akiyoshi
APPLICANT: Ichimori, Yuzo
TITLE OF INVENTION: Method For Assaying MAP Kinase
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                   ; OTHER INFORMATION: EGFP-Erkl fusion construct
US-09-417-197-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRPIFPGKHYLDQLNHIL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 KELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 KELIFQETARFQPGVLEAP 631
                                 ORGANISM: Artificial Sequence
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LENGTH:
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Sequence 57, Application US/09417197

Sequence 57, Application US/09417197

Patent No. 6518021

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP, et al.

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT:

TITLE OF INVENTION: On A Cellular Response

FILE REFERENCE: 3759-0110P

CURRENT PILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SEQ ID NO 57

LENGTH 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 NRPIFPGKHYLDOLMHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 SKALDLIDRMLTFNPNKRITVAAALAHPYLEQYYDPTDEPVAEEPPTFAMELDDLPKERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRRFRHENVIGIRDILRASTLEAMRDVYI
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                                                                                                                                                                                                                                                                                                                                                                                              Length 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                         97.5%; Score 1719; DB 2;
87.9%; Pred. No. 2.2e-172;
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FILING DATE: 28-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: TOODBY, Kimberlin M.
RECISTRATION NUMBER: 35,391
REFERENCE/OCKET NUMBER: 04221.0039-00000
TELECOMMUICATION INFORMATION:
TELEPHONE: (202)408-4000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: MERK1-F64L-S65T-GFP fusion US-09-417-197-57
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRPIFPGKHYLDQLNHI
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.5
Best Local Similarity 87.9
Matches 333; Conservative
                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                   US-08-622-277A-8
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Gaps

252

268

us-10-623-108-2.rai

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269 FNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ 328
                                                                                                                                                                                                                                 73 ISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKL 132
                                                                                                                                                                                                                                                      61 ISPFEHQTYCQRTLREIQILLGFRHENVIGIRDILRAPTLEAMRDVYIVQDLMETDLYKL 120
                                                                                                                                                                                                                                                                                                                133 LKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIAD 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 EPRRITEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKK 72
                                                                                                                                                                           193 PEHDHIGFLIEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 QLNHIL-----ALDILDRMLT
                                                                                                              44;
                                                                    Length 367;
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Patent No. 587206

GENERAL INFORMATION:
APPLICANT: Cobb, Melanie H.
APPLICANT: Cobb, Melanie H.
APPLICANT: Nye, Steven
APPLICANT: Nye, Steven
APPLICANT: Nye, Steven
TITLE OF INVENTION: A Family of Map2 Protein Kinases
CORRESPONDENCE 21

CORRESPONDENCE 21

CORRESPONDENCE Pennie & Edmonds

STREET: 1155 Avenue of the Americas
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/176,620
PRIOR APPLICATION NUMBER: US 08/176,620
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRANCE/DOCKET NUMBER: 18,872
REGISTRANCE/DOCKET NUMBER: 6526-123
                                                                      Score 1607; DB 1;
Pred. No. 1.3e-160;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: 6526-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    Query Match 91.2%;
Best Local Similarity 85.3%;
Matches 313; Conservative 3
              , MOLECULE TYPE: protein US-08-176-620A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
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unknown
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10036
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ZIP: 1003
TOPOLOGY:
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                                                                                                                                                                                                                                         ICDFGLARIADPEHDHTGFLTEYVATRWYRAPBIMLNSKGYTKSIDIWSVGCILAEMLSN 241
                                                                                                                                                                                                                                                                                                                                                                                   -ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 KALDILDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFDMELDDLFKERLK 362
                                                                                                                                   HVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIV 121
                                                                                                                                                            QDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLK 181
                                                                                                                                                                                                                                                                                                                                                                                                                      243 RPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDS 302
                                                          61
                                                                               3 AAAAAPGGGGEPRGTAGVVPVVPGEVEVVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD 62
                                                        2 AAAAAQGGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD
                    44; Gaps
                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION: 800
CLASSIFICATION: 800
85.4%; Pred. No. 9.7e-166;
tive 1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08176620A; Patent No. 5595904; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/POCKET VUMBER: 6526.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELIPQETARFOPGAPEGP 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: single
                Matches 323; Conservative
Best Local Similarity
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US-08-176-620A-11
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61 TLREIQILLERFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 YFLYQILRGLKYHHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 PGEVEMVKGOPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.1%; Score 1606; DB 2; Length 355; 87.6%; Pred. No. 1.6e-160; ive 0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASE, SEQUENCES, AND METHODS OF PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street:
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lechner, Cornelia Moller, Niels P.H. Ulrich, Axel Ulrich, Axel TITLE OF INVENTION: EXTRACELLULAR
US/08/459,953A
           FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 209/267
TELEPHONE: (213) 499-1600
TELEPHONE: (213) 499-1600
TELEPHONE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-393-212-8; Sequence 8, Application US/09393212; Patent No. 6739972; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                          : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 87.6
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                         US-08-459-953A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 FNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 FNPKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFDMELDDLPKERLKELIFQETARFQ 360
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                                                                                                                                                                                                                                                                                                                       1 EPRGTAGVVPVVPGEVEVVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 PEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLD
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                            Length 367;
                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08459953A
Sequence 8, 6030822
GENERAL INFORMATION:
APPLICANT: Lechner, Cornelia
APPLICANT: Moller, Niels P.H.
APPLICANT: MOllrich, Axel
TITLE OF INVENTION: EXTRACELLULAR SIGNAL-RELATED
TITLE OF INVENTION: METHODS OF PRODUCTION
TITLE OF INVENTION: METHODS OF PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          91.2%; Score 1607; DB 1;
85.3%; Pred. No. 1.3e-160;
tive 1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 9001-2066
COMFUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Callfornia
 : (212) 790-9090
(212) 869-8864/9741
                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
                                                                                                                                                                                                                                             Best Local Similarity 85.3
Matches 313; Conservative
                                                                                                                             STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
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                                                                                                              TYPE: amino acid
 TELEPHONE:
TELEFAX: (2
TELEX: 6614
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US-08-459-953A-8
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255 NHIL-----ALDLLDRMLTFN 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 PNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQPG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 HDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQL 254
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90.5%; Score 1595; DB 1; Length 365;
Best Local Similarity 85.2%; Pred. No. 2.4e-159;
Matches 311; Conservative 1; Mismatches 9; Indels 4
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Patent No. 5776751
GENERAL INFORMATION:
APPLICANT: BOULton, Teri G. et al.
TILLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                           COMPUTER: TELEPPY disk
COMPUTER: TIBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELEPPAN: (212) 790-9090
TELEPPAN: (212) 780-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-08-463-862-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 PGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
CORRESPONDENCE: 21
               SCOMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,212
FILING DATE: 09-Sep-1999
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 08/459,953A
FILING DATE: JUNE 2, 1995
APPLICATION NUMBER: 08/029,494
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburgy, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELEFRONDING (213) 499-1600
TELEFRAX: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: G--SED NO: 8:
SEQUENCE CHARACTERISTICS:
  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08176620A Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Cobb, Melanie H. APPLICANT: Yancopoulos, George D. APPLICANT: Yancopoulos, George D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-176-620A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADFE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 RRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS
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90.5%; Score 1595; DB 1; Length 365;
Best Local Similarity 85.2%; Pred. No. 2.4e-159;
Matches 311; Conservative 1; Mismatches 9; Indels 4
                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DUS/NS-DUS
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/463,862
FILING DATE: 05-UN-1995
CLASSIFICATION NUMBER: US/08/463,862
FILING DATE: 05-UN-1995
CLASSIFICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REFERENCE/DOCKET NUMBER: 6226-049
TELEFONNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TENGRAL 34E AMINO ACIGAR
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
          STREET: LITTER New York
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Sequence 2, Application US/08461985; Patent No. 5872006; GENERAL INFORMATION: APPLICANT: BOULton, Teri G.

RESULT 15 US-08-461-985-2

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271 PNKKITVERALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQPG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HDHTGFLFEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 RRIEGVGPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
   APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Yancopoulos, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                  COMPUTER KEADABLE FORM:
COMPUTER: LEAP PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US/08/176,620
PRIOR APPLICATION NUMBER: US 08/176,620
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,94
ATTORNEY/AGENT NUMBER: 18,97
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.5%; Score 1595; DB 1;
85.2%; Pred. No. 2.4e-159;
iive 1; Mismatches 9;
                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
Cobb, Melanie H.
Yancopoulos, George D.
Nye, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-8864/9:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.2
Matches 311; Conservative
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                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                   New York
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                                                                                                                                                                  CITY: Nev
STATE: Ne
COUNTRY:
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Sequence 2, Applisequence 14, Applisequence 19, Applisequence 19, Applisequence 2, Applisequence 25, Applisequence 25, Applisequence 25, Applisequence 25, Applisequence 39, Applisequence 110, Applisequence 127, Applisequen
                                                                                                                                                     February 6, 2006, 15:35:46; Search time 116.816 Seconds (without alignments) 1198.238 Million cell updates/sec
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                                                                                                                                                                                                                                                            US-10-623-108-2
1763
1 MAAAAAQGGGGEPRRIEGV......LKELIFQETARFQPGVLEAP 335
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/cgn2_6/ptcdata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-234-48-7
US-10-234-48-14
US-10-394-322A-19
US-10-70-78-18-3
US-10-735-118-3
US-10-623-108-6
US-10-653-108-6
US-10-659-585-37
US-10-659-585-37
US-10-10-663-25
US-10-10-663-25
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US-10-10-63-25
US-10-10-10-89
US-10-623-108-8
US-10-623-108-8
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US-10-114-270-110
US-10-114-270-110
US-10-132-923-1420
US-10-114-270-115
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US-10-31-882-215
US-10-31-888-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA Main:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1867569 segs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
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34.5 81.4 358 5 US-10-451-291B-10 Sequence 10, Appl 34.5 81.4 604 4 US-10-072-036-59 Sequence 59, Appl 34.5 81.4 605 4 US-10-072-036-41 Sequence 59, Appl 1423 81.3 369 5 US-10-732-923-1421 Sequence 1421, Appl 1426 80.9 355 5 US-10-732-923-1421 Sequence 19, Appl 1424 80.8 346 5 US-10-941-65-19 Sequence 19, Appl 1424 80.8 360 4 US-10-756-19-19-19-19-19-19-19-19-19-19-19-19-19-	ALIGNMENTS	RESULT 1  US-10-623-108-2  Sequence 2, Application US/10623108  Publication No. US20050013817A1  GENERAL INFORMATION:  APPLICANT: DAI, KEN-SHWO  TITLE OF INVENTION: HUMAN SWAPK3-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS  FILE REPERENCE: US/10/623,108  CURRENT APPLICATION WUMBER: US/10/623,108  CURRENT FILING DATE: 2003-07-18  NUMBER OF SEQ ID NOS: 8  SOFTWARE: Patentin version 3.1  LENGTH: 335  TYPE: PRT  CORGANISM: Homo sapiens  US-10-623-108-2	itch 100.0%; Score 1763; DB 5; Length 335; sal Similarity 100.0%; Pred. No. 1e-136; 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MAAAAAQGGGGGEPRRTEGV 	61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVXI 120 	121 VODLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180 	181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240 	241 NRPIFPGKHYLDQLNHILALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEE 300 	301 PFTFAMELDDLPKERLKELIFQETARFQPGVLEAP 335 	448-7 9 7. Application US/10233448
28 1434. 29 1434. 30 1434. 31 1423. 32 1415. 34 1415. 36 1415. 37 137 137 137 137 137 137 137 137 137 1		RESULT 1 US-10-623-108- ; Sequence 2, ; Publication ; GENERAL INFC APPLICANT: ; TITLE OF IN ; FILE REPRER ; CURRENT APP; ; CORGANISM: ; CROGANISM: ; CROGANISM: ; CROGANISM: ; CROGANISM: ; CROGANISM: ; CROGANISM:	Query Match Best Local Matches 33		Qy 61 Db 61	Oy 121 Db 121	18	Qy 241 Db 241	Qy 301 Db 301	RESULT 2 US-10-233-448 ; Sequence 7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VODLMETDLYKLLKSOOLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 NRPIFFGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ALDLLDRMLTENDNKRITVERALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
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                                                                                                                                                                                                                                                                                                                                                                                      1 MAAAAAQGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                       APPLICANT: Fisone, Gilberto
TITLE OF INVENTION: METHOD FOR CLASSIFICATION OF ANTI-PSYCHOTIC DRUGS
FILE REFERENCE: 11181-009
CURRENT APPLICATION NUMBER: US/10/233,448
CURRENT FILING DATE: 2001-09-03
PRIOR APPLICATION NUMBER: 60/316,338
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8
SOFTWARR: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/10174794
; Sequence 14, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
    APPLICANT: University of Southern California
    TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
    TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-708;
    CURRENT APPLICATION NUMBER: US/10/174,794
    CURRENT FILING DATE: 1999-10-01
    PRIOR PILING DATE: 1999-10-01
    PRIOR PLILING DATE: 1999-10-01
    PRIOR PLILING DATE: 1999-10-01
    PRIOR PLILING DATE: 1999-10-01
    NUMBER OF SEQ ID NOS: 16
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                 Length 379;
                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                Query Match 98.2%; Score 1731; DB 4; Best Local Similarity 88.4%; Pred. No. 5.2e-134; Matches 335; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 KELIFOETARFOPGVLEAP 335
Publication No. US20030109419A1
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRPIFPGKHYLDQLNHIL
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TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-10-174-794-14
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                                                                                        1 MAAAAAQGGGGGBPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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        Score 1731; DB 4; Length 379; Pred. No. 5.2e-134;
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Sequence 19, Application US/10394322A

Sequence 19, Application US/10394322A

PUBLICATION NO. USZO030232391A1

GENERAL INFORMATION:

APPLICANT: SUNESIS PHARMACEUTICALS, INC.

TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS

FILE REFERENCE: 39750-0006 US

CURRENT PELICATION NUMBER: US/10/394,322A

CURRENT FILING DATE: 2003-03-20

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19

LENGTH: 379

LENGTH: 379

LENGTH: 379

CORGANISM: Homo sapiens

US-10-394-322A-19
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Pred. No. 5.2e-134;
0; Mismatches 0;
98.2%; Score ... 5.2e-1
88.4%; Pred. No. 5.2e-1
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Best Local Similarity 88.4%;
Matches 335; Conservative
                                                  Matches 335; Conservative
                               Best Local Similarity
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181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                          241 NRPIFPGKHYLDOLMHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                          259 --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
                                                                                                                                                                                                                                                       Sequence 8, Application US/10701490

Publication No. US20040106141A1

GENERAL INFORMATION

APPLICANT: PAUL S. MISCHEL

APPLICANT: GRARLES L. SAWYERS

APPLICANT: GRARLES L. SAWYERS

APPLICANT: GRARLEY L. SANTTH

APPLICANT: RATHERINE CROSBY

TITLE OF INVENTION: PATHWAYS ASSOCIATED WITH GLIOBLASTOWA PROGRESSION

TITLE OF INVENTION: PATHWAYS ASSOCIATED WITH GLIOBLASTOWA PROGRESSION

CURRENT APPLICATION NUMBER: US/10/701,490

CURRENT PILING DATE: 2003-11-05

PRIOR APPLICATION NUMBER: 60/423,777

PRIOR APPLICATION NUMBER: 60/423,777

SOFTWARE: PASESQ ID NOS: 11

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 379
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Matches 335; Conservative
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ORGANISM: Homo Sapiens
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US-10-701-490-8
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RESULT

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Sequence 3, Application US/10735118

Publication No. US20040248151A1

GENERAL INFORMATION:

APPLICANT: Bacus, Sarah S.

TITLE OF INVENTION: WETHOO FOR PREDICTING THE RESPONSE TO HER2-DIRECTED THERAPY

FILE REFERENCE: 6270-701.201

CURRENT FILING DATE: 2003-12-11

PRIOR FILING DATE: 2002-04-05

PRIOR PELICATION NUMBER: US 60/432,943

PRIOR FILING DATE: 2003-04-07

PRIOR PELING DATE: 2003-04-07

PRIOR PELING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 379

TYPE: PRI

CORRANISM: Homo sapiens
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Pred. No. 5.2e-134;
0; Mismatches 0;
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US-10-623-108-6
Sequence 6, Application US/10623108
Sequence 6, Application US/10623108
Sequence 6, Application US/10623108
Sequence 7
Sequence 8
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Best Local Similarity 88.4%;
Matches 335; Conservative
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APPLICANT: Shin-Ichi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Chiaki Senoo
APPLICANT: Oun-Ichi Nozu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
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                           241 NRPIFPGKHYLDÓLNHÍLGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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                                                          259 --ALDLIDRMITFNPNKRITVBEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
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Pred. No. 1.6e-133;
0; Mismatches 1;
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; Sequence 16, Application US/10060065
; Publication No. US20030017480A1
; GENERAL INFORMATION:
                                                                                                                                                KELIFQETARFQPGVLEAP 335
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Best Local Similarity 88.1%;
Matches 334; Conservative (
241 NRPIFPGKHYLDQLNHIL
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Shizuko Ishii
                                                                                                                                                                                                                                                                                                                                                                                                              Tomoyasu Sugiyama
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APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
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Keiichi Nagai
Tetsuji Otsuki
                                                                                                                                                                                                                                                                                                                                                            Kaoru Otsuka
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APPLICANT:
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APPLICANT:
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                              98.2%; Score 1731; DB 5; Length 379;
88.4%; Pred. No. 5.2e-134;
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Publication No. US20050095657A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Methods and Kits for Detecting Proteins
FILE REFERENCE: 50508-228
CURRENT APPLICATION NUMBER: US/10/945,684
CURRENT FILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
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Pred. No. 5.2e-134;
0; Mismatches 0;
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Best Local Similarity 88.4%;
Matches 335; Conservative
                                                                 Matches 335; Conservative
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; ORGANISM: Homo Sapiens
US-10-945-684-2
                                              Best Local Similarity
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US-10-623-108-6
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US-10-945-684-2
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301 SKALDLLDRMLTFNPNKKITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 360
                    259 --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Germann, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
Serine/Thereonine Kinases and Tyrosine Kinase
                                                                       KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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88.1%; Pred. No. 1.6e-133;
iive 0; Mismatches 1; Indels 44
                                                                                                                                                 NRPI PPGKHYLDQLNHIL------
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: VPI 97-104 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/170,663
FILING DATE: 12-Jun-2002
CLASSIFICATION: <Unknown>
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-170-663-25
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APPLICATION NUMBER: 09/025,580
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, Keith Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/10170663
Publication No. US20030165899A1
GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
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TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 88.1:
Matches 334; Conservative
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US-10-170-663-25
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                                                                                                                                                                              --ALDLLDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAERPFTFAMBLDDLPKERL 316
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    KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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Pred. No. 1.6e-133;
0; Mismatches 1;
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APPLICANT: Punahashi, Shin-Ichi
APPLICANT: Seno, Chiaki
APPLICANT: Nezu, Jun-Ichi
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
PRIOR PLLING DATE: 2000-07-28
PRIOR PLLING DATE: 2000-07-28
PRIOR PLLING DATE: 2000-02-17
PRIOR PLLING DATE: 1000-02-17
PRIOR PLLING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/189,590
PRIOR APPLICATION NUMBER: US 60/189,590
PRIOR PLLING DATE: 1999-10-18
PRIOR PLLING DATE: 2000-01-11
PRIOR PLLING DATE: 2000-01-11
PRIOR PLLING DATE: 2000-05-02
PRIOR PLLING DATE: 2000-05-02
PRIOR PLLING DATE: 1999-07-29
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
                                                                             NRPI FPGKHYLDQLNHIL-----
                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/10059585 Publication No. US20030082776A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                            KELIFQETARFQPGVLEAP 335
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Best Local Similarity 88.1%;
Matches 334; Conservative C
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Ishii, Shizuko
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Wakamatsu, Ai
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ota, Toshio
APPLICANT: 1809ai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
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Otsuki, Tetsuj
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US-10-059-585-37
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Sequence 39, Application US/10072036

| Sequence 39, Application US/10072036
| Sequence 39, Application No. US20030082564A1
| GENERAL INFORMATION:
| APPLICANT: Old THASTUD
| APPLICANT: Soren TULIN
| APPLICANT: Soren TULIN
| APPLICANT: Match SCUDDER
| TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT FILE THE PROPERTY APPLICATION NUMBER: US/10/072,036
| CURRENT FILING DATE: 1999-11-07 |
| NUMBER OF EXQ. ID NOS: 1433 |
| NUMBER OF EXQ. ID NOS: 1433 |
| NUMBER OF EXQ. ID NOS: 1433 |
| NUMBER OF EXC. ID NOS: 1433 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
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                                                                                                                                                                                                                                                                                                                                                            VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
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                                                                                                                                                                                                                                                                                                                             1 MAAAAAQGGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                           Length 379;
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                                                                                                                                                                                                                                                                   1; Indels
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Best Local Similarity 88.1%; Pred. No. 3e-133;
Matches 334; Conservative 0; Mismatches 1;
                                                                                                                                                                                                     Score 1725; DB 5;
Pred. No. 1.6e-133;
0; Mismatches 1;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
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SEQ ID NO 39
LENGTH: 631
                                                                                                                                                                                                           Query Match
Best Local Similarity 88.1%;
Matches 334; Conservative (
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ORGANISM: Artificial Sequence
                                                                                                                                                US-10-893-072-25
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US-10-072-036-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 SKALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 360
                                                                                                                                                       DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                   KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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Wilson, Keith Phillip
Wilson, Ursula A.
Germann, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/642,749
FILING DATE: 18-Aug-2000
APPLICATION NUMBER: US/09/025,580
FILING DATE: «Unknown»
ATTORNEY/AGNT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/893,072
FILING DATE: 15-Jul-2004
CLASSIFICATION: <UNKNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRPIFPGKHYLDQLNHIL
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US-10-893-072-25
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                                                                                                                                           259 -ALDLLDRMLTFNPNKRITVERALAHPYLEQYYDPTDGPVAEEPFTFAMELDDLPKERLK 317
                                                                              243 RÞÍFÞGKHYLDÓLNHÍLGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDS 302
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91.1%; Score 1606; DB 4; Length 355;
Best Local Similarity 87.6%; Pred. No. 9.4e-124;
Matches 311; Conservative 0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ullrich, Axel
TITLE OF INVENTION: EXTRACELLULAR SIGNAL-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Microsoft word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/461,402
FILING DATE: 16-Jun-2003
CLASSIFICATION NUMBER: US/08/459,953A
APPLICATION NUMBER: US/08/459,953A
FILING DATE: J995
FILING DATE: J995
APPLICATION NUMBER: 08/029,494
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
RESERRINGE/DOCKET NUMBER: 32,327
FELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINASE, SEQUENCES, AND METHODS OF PRODUCTION
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10461402
Publication No. US20030229209A1
GENERAL INFORMATION:
APPLICANT: Lechner, Cornelia
Moller, Niels P.H.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
Suite 4700
                                                                                                                                                                                                                                                                       318 ELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                                                                                                              AND USE
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INFORMATION FOR SEQ ID NO: 8 :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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APPLICANT: Kasper ALAMHOLT
APPLICANT: Kasper ALAMHOLT
APPLICANT: Kasper ALAMHOLT
APPLICANT: Kasper ALAMHOLT
APPLICANT: Witt SCUDDER
TITLE OF INVENTION: On A Cellular Response
FILE REPERENCE: 3759-0120P
FILE REPERE
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                                                       373 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL 432
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                                                                                                                                                                                  VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                              KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                           -- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ALDLLDRMLTFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
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253 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY 312
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Pred. No. 8e-128;
1; Mismatches 10; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         NRPI FPGKHYLDQLNHIL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MERK1-F64L-S65T-GFP fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 57, Application US/10072036; Publication No. US20030082564A1; GENERAL INFORMATION: APPLICANT: Ole THASTRUP
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Best Local Similarity 85.4%;
Matches 323; Conservative
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ORGANISM: Artificial Sequence
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LENGTH: 624
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1 PGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR 60	85 TLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHIC 144	61 TLREIQILLRFRHENVIGIRDILRASTLEAMRDVYLVQDLMETDLYKLLKSQQLSNDHIC 120	145 YFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADFEHDHTGFLTEY 204	121 YFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEY 180	205 VATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHIL 258	181 VATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSP 240	259	241 SQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEA 300	281 LAHPYLEQYYDFIDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQPGVLEAP 335	=
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Search completed: February 6, 2006, 15:40:56 Job time : 117.816 secs

269, App 8, Appli 273, App 9, Appli 10, Appl

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US-11-024-959-386 US-11-024-959-391 US-10-770-726-52 US-11-024-959-266 US-11-024-959-268

ALIGNMENTS

267, App 72, Appl 65, Appl 5, Appli 5, Appli 261, App 269, App

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US-11-113-424-183 US-11-024-959-267 US-10-770-726-65 US-11-024-959-385 US-11-024-959-271 US-11-024-959-271 US-11-024-959-261 US-11-024-959-269 US-11-024-959-269 US-11-024-959-273 US-11-024-959-273 US-11-024-959-273 US-11-024-959-273 US-11-024-959-273 US-11-024-959-273 US-11-024-959-273

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APPLICANT: Al Wakamat Sugiyama
APPLICANT: Teteuji Otsuki
APPLICANT: Chiaki Senoo
APPLICANT: Uun-1chi Nezu
TITLE OF INVENITION: NUMBER: US/11/109,156
CURRENT APPLICATION NUMBER: US/10/060,065
PRIOR PLILING DATE: 2000-07-29
PRIOR PLILING DATE: 2000-07-29
PRIOR PLILING DATE: 2000-07-29
PRIOR PLILING DATE: 2000-07-29
PRIOR PLILING DATE: 1999-07-29
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 43
SSOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/11109156
Publication No US20050250144A1
GENERAL INFORMATION:
APPLICANT: Takao Ioogai
APPLICANT: Takao Ioogai
APPLICANT: Tetsuo Nishikawa
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Jun-Ichi Yamamoto
Shizuko Ishii
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; LENGTH: 379
; TYPE: PRT
ORGANISM: Homo sapiens
US-11-109-156-16
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      February 6, 2006, 15:37:06; Search time 10.1369 Seconds (without alignments) 387.254 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW FUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW FUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US07 NEW FUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT NEW FUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10 NEW FUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US11 NEW FUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US11 NEW FUB.pep:*
                        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-878-556A-134

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US-10-870-726-69

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US-11-127-817-19

US-11-127-817-19

US-11-127-817-19

US-11-024-959-265

US-11-024-959-265

US-11-024-959-264

US-11-024-959-264

US-11-024-959-264

US-11-024-959-264

US-11-024-959-264

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US-11-109-156-11
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US-11-024-959-395
US-11-024-959-393
US-11-024-959-270
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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APPLICANT: BERGET, Allison

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APPLICANT: Berger, Allison

APPLICANT: Guillemette, Tracy L.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION NUMBER: US/10/301,822

PRIOR PLILING DATE: 2002-01-21

PRIOR PLILING DATE: 2002-11-210

PRIOR PLILING DATE: 2002-11-210

PRIOR PLILING DATE: 2002-11-210

PRIOR PLILING DATE: 2002-12-10

PRIOR FILING DATE: 2002-05-20

NUMBER: GENT OF MINDER: US 60/381,988

PRIOR FILING DATE: 2002-05-20

NUMBER: FBEEN SEQ ID NOS: 228

SOFTWARE: FBEEN SEQ ID NOS: 228

SOFTWARE: FBEEN SEQ ID NOS: 228

SEQ ID NO 115

LENGTH: 360

MANNER OF SEG ID NOS: 228

SEQ ID NO 115

LENGTH: 360
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                                                              224 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNAD
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                                                                                                                           --ALDLLDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL
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                                                                                                                                                                                                                                                                                                                                                                  US-11-186-284-115
; Sequence 115, Application US/11186284
; Publication No. US20050266493A1
; Publication No. WS20050266493A1
; PublicANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 NRPIFPGKHYLDQLNHIL-----
                                                                                                                                                                                                                        317 KELIFQETARFQPG 330
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344 KELIFEETARFQPG 357
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CORGANISM: Homo Sapiens
US-11-186-284-115
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                                                                                                                                                                                                    120
                                                                                                                                                                                                                                            61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                            121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYHSANVLHRDLKPSNLLSNTTCDL 180
                                                                                                                                                                                                                                                                                                                                                                                                181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 --ALDLLDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 SKALDLIDRMLIFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 360
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                                                                                                                                                    1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                    1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVENVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                       Gaps
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                                                       44;
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       Length 379;
                                                       Indels
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APPLICANT: Hoffmann La-Roche Inc.; TITLE OF INVENTION: HCV regulated protein expression; FILE REFERENCE: 21762; CURRENT APPLICATION NUMBER: US/10/878,556A; CURRENT FILING DATE: 2004-06-28; NUMBER OF SEQ ID NOS: 199; SOFTWARE: PatentIn version 3.1; SEQ ID NO 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
Score 1725; DB 7;
Pred. No. 5.3e-147;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.9%; Score 1444.5; DB 6
Best Local Similarity 74.3%; Pred. No. 6.1e-122;
Matches 278; Conservative 18; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/mk01_human
DATABASE ENTRY DATE: 1992-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRPIFPGKHYLDQLNHIL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 KELIFQETARFQPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 KELIFQETARFOPGVLEAP 379
  Query Match 97.8%;
Best Local Similarity 88.1%;
Matches 334; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-878-556A-134
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GENERAL INFOGRATION:
ADPLICANT: ROTH, RICHARD B.
APPLICANT: ROTH, RICHARD B.
APPLICANT: RAWRERER, STEFAN M.
APPLICANT: RAWRERER:
APPLICANT: RAWRERER:
APPLICANT: RENELAND, MATTHEW ROBERS;
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: WHETHOOS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS;
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: 10/723,681
PRIOR PILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
SEQUENTE ELUNG APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
SEQUENTE FILING DATE: 2003-11-25
SEQUENTE APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 IGIRDILR-ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 ANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTBYVATRWYRAPEIMLNS 219
                                                                                                                                                                                                                                                                                                                                                                                                     42 YTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLRFRHENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 YVSPTHVGSGAYGSVCSAIDKRSGEKVAIKKLSRPFQSEIFAKRAYRELLLLKHMQHENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 ------ALDLIDRMLTFNPNKRITVEEALAHPYLEQYYDPTDE
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                                                                                                                                                                                                                                                                                        Length 365;
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                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 KGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHIL----
                                                                                                                                                                                                                                                                                        ; Score 678.5; DB 6;
; Pred. No. 2e-53;
55; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 PVAEEPFTFAMELDDLPKERLKELIFQETARFQP 329
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CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 69
LENGTH: 365
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-10-770-726-69
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Best Local Similarity 41.6%;
Matches 139; Conservative 5:
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Matches 133, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. USZU
GENERAL INFORMATION:
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Publication No. US20050266409A1
ABDELICANT: NYeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVATRWYRAP 213
            --ALDLLDRMLTFNPNKRITVBEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKBRL 316
                                             284 SKALDLIDKMLTFNPHKRIEVEQALAHPYLEQYYDPSDEPIAEAPFKFDMELDDLPKEKL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLR
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Deciphera Pharmaceuticals, Inc.
APPLICANT: Deciphera Pharmaceuticals, Inc.
APPLICANT: Flynn, Daniel L
APPLICANT: Petillo. Peter A
17TLE OF INVENTION: Anti-Inflammatory Medicaments
FILE REFERENCE: 34477-CIP
CURRENT APPLICATION NUMBER: US/10/886,329
CURRENT APPLICATION NUMBER: US 60/437,415
PRIOR PILING DATE: 2004-07-06
PRIOR PILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2003-12-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.4%; Score 747.5; DB 6; Best Local Similarity 45.1%; Pred. No. 1.3e-59; Matches 155; Conservative 55; Mismatches 81;
                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/10886329; Publication No. US20050288286A1; GENERAL INFORMATION:
                                                                                                                                 KELIFQETARFQPG 330
                                                                                                                                                               ORGANISM: Homo sapiens
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US-10-770-726-69
                                                                                                                                                                                                                                                                            RESULT 4
US-10-886-329-1
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291 QPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISV 350
                                                 35.2%; Score 620; DB 7; Length 42
38.2%; Pred. No. 4.3e-48;
ive 67; Mismatches 80; Indels
                                                                                                                                    ; Sequence 20, Application US/11127817; Publication No. US20050287519A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 38.23
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-11-127-817-20
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US-11-127-917-18
US-11-127-917-18
Sequence 18, Application US/11127817
Publication No. US20050287519A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Merchiers, Pascal G.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wends,
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT APPLICATION NUMBER: 05/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-06-12
PRIOR FILING DATE: 2004-06-12
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SCOTTAND NOS: 534
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   FDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLR 94
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Best Local Similarity 38.2
Matches 133; Conservative
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APPLICANT: Marchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: 05/11/127,817
CURRENT FILING DATE: 2005-05-12
FRIOR FILING DATE: 2004-05-12
FRIOR FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: Patentin Version 3.3
SEQ ID NO 200
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US-11-127-817-19
US-11-127-817-19
Sequence 19, Application US/11127817
Publication No. US20050287519A1
GENERAL INFORMATION:
APPLICANT: Merchiere's Peacal G.
APPLICANT: Apfitacls, Koenraad F. F.
APPLICANT: Spittacls, Koenraad F. F.
APPLICANT: Spittacls, Compositions And Compound Assays For Inhibiting TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting; TITLE OF INVENTION: Amyloid-Beta Protein Production
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118 CHSHRVIHRDIKPONILIDRRINSIKLADFGLAR-----AFGIPVRTFTHEVVTIM 168
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                                                                                                                                         63 IVKLQDVVHSE-----RRLYLVFEYLDLDLKKGMDSCPEFSKDTHTIKMFLXQILRGISY 117
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                                                            Indels 57; Gaps
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APPLICANT: CONNETT, MARIE B.
APPLICANT: CONNETT, MARIE B.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERGON, SARAH JANE
APPLICANT: HIGGIOR, MURRAY ROBERT
APPLICANT: HIGGIOR, MURRAY ROBERT
APPLICANT: HIGGIOR, MURRAY ROBERT
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: KODEXZKKI, BOB
ITILE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044623.036
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: GO/533,036
PRIOR PLILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PARCENTIN VERSION 3.3
SEQ ID NO 262
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.3%; Score 464.5; DB 7; 35.6%; Pred, No. 2.2e-34;
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45; Mismatches
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Publication No. US20060010516A1
GENERAL INFORMATION:
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Best Local Similarity 35.65
Matches 105; Conservative
  108; Conservative
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291 QPTVRNYVENRPKYAGLTFPKLFPDSELNKLKASQARDLLSKMLVIDFAKRISV 350
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                                                                                                                                                                                                                                                                                                                Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FORETH, RICHARD L.
APPLICANT: FORETH, RARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGGOR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: MAGNISIN, AND TROY
APPLICANT: MONEXYEM, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
                                                                                                                                                                                                                                                                                                                                                     80; Indels
                                                                                                                                                                                                                                                                                                          $; Score 620; DB 7;
$; Pred. No. 4.8e-48;
67; Mismatches 80;
               CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR PILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR PILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SEQ ID NO 19
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PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentIn version 3.3
SEQ ID NO 263
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 263, Application US/11024959; Publication No. US20060010516A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.3%;
36.0%;
                                                                                                                                                                                                                                                                                                              35.2%;
38.2%;
      FILE REFERENCE: P27,800-D USA
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 38.2
Matches 133; Conservative
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ORGANISM: Eucalyptus sp.
                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-127-817-19
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Best Local Similarity
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                                                                                                                                                                                                       LENGTH: 464
TYPE: PRT
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NUMBER OF SEQ ID NOS: 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 VVRIHDVIHTN-----KKLILVFEFVDYDLKKFLHNFDKGIDPKIVKSLLYQLVRGVAHC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 HSANVLHRDLKPSNLLINTTCDLKICDFGLAR-IADPEHDHTGFLFEYVATRWYRAPEIM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 RYTOLOYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCORTLREIQILLRFRHEN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 -----ALDILIDRMIJTENPNKRITVEEALAHPYLEQYYD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 DWKPENFEKYPGEPLNKVCPKMDPDGLDLLDKMLKCNPSERIAAKNAMSHPYFKDIPD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :|: :||| ||:| | | | | ||:||| | ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
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                                                                                                                                             Sequence 264, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INPORMATION:
    APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONSTER, RICHARD L.
; APPLICANT: CONSTER, RICHARD L.
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGIS, COLLEEN M.
; APPLICANT: HIGGIS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: CONSTER, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: CONSTERCE: 04463-036
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 04463-036
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PATENTIN VERSION 3.3
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APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTIVE OF INCELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
RIGH APPLICATION NUMBER: 60/533,036
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
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Publication No. US20060010516A1
GENERAL INFORMATION:
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APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGOR, WURRAY ROBERT
APPLICANT: LUND, STEVEN TROY
APPLICANT: MAGUSIN, ANDREAS
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CRGANISM: Eucalyptus sp.
US-11-024-959-264
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Best Local Similarity
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US-11-024-959-265
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LENGTH: 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| :|||| || || || : 229 PGVTALPDFKSAFPKWPAKNLQDMVPGLNSAGIDLLSKMLCLDPSKRITARSALEHEYFK 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 CHSHRVLHRDLKPONLLIDRRTNALKLADFGLAR-----AFGIPVRTFTHEVVTLW 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ALDLLDRMLTFNPNKRITVEEALAHPYLE 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 VIGIRDILRASTLEAMRDVYIVQDLMETDLYKLL-KSQQLSNDH--ICYFLYQILRGLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 IHSANVLHRDLKPSNLLIN-TTCDLKICDFGLARIADPEHDHTGF-----LTEYVATRW
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                                                                                                                                                                                                                                                                                                                              Length 294;
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| GENERAL INFORMATION: USZUOGOUIOSIGAI
| APPLICANT: CONNETT, MARIE B.
| APPLICANT: CONNETT, MARIE B.
| APPLICANT: EMERSON, MURRAY ROBERT
| APPLICANT: HIGGINS, COLLEEN M.
| APPLICANT: HIGGINS, COLLEEN M.
| APPLICANT: MAGISIN, ANDREAS
| APPLICANT: KODRZYCKI, BOB
| TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
| TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
| FILE REFERENCE: 044465-0360
| CURRENT FILING DATE: 2004-12-30
| PRIOR PELING DATE: 2003-12-30
| PRIOR PELING DATE: 2003-12-30
| NUMBER OF SEQ ID NOS: 782
| SEQ ID NO 384
| LENTHER DATE: MORE NOS: 782
| SEQ ID NO 384
| LENTHER DATE: DA
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  26.1%; Score 460.5; DB 7;
35.7%; Pred. No. 4.8e-34;
ive 45; Mismatches 81;
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; Sequence 384, Application US/11024959
; Publication No. US20060010516A1
SOFTWARE: Patentin version 3.3
SEQ ID NO 265
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 35.74
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.8
Best Local Similarity 35.1
Matches 104; Conservative
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 YTQLQYIGEGAYGWVSSAYDHVRKTRVAIKKI-SPFEHQTYCQRTLREIQILLRFRHENV 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 YQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVAT 207
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                                                     213 PEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHIL------- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ALDLLDRMLTFNPNKRITVEEALAHPY 285
                                                                                                                                            Query Match
25.6%; Score 450.5; DB 7; Length 520;
Best Local Similarity 33.6%; Pred. No. 8e-33;
Matches 118; Conservative 53; Mismatches 105; Indels 75; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 --AEYFWADPLPCDPKSLPKYESSHEFQTK----KKRQQQRQHEETAKRQ 364
                                                                                                                                                                                                                           US-11-024-959-272

Sequence 272, Application US/11024959

Publication No. US20060010516A1

GENERAL INFORMATION

APPLICANT: CONNETT, WARIE B.

APPLICANT: GRIGGON, SARAH BN.

APPLICANT: GRIGGON, GRAH JANE

APPLICANT: HIGGINS, COLLEEN M.

APPLICANT: HIGGINS, COLLEEN M.

APPLICANT: HIGGINS, COLLEEN M.

APPLICANT: HOUD, STEVEN TROY

APPLICANT: KODRZYCKI, BOB

TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS

FILE REPERENCE: 044463-0360

CURRENT FILING DATE: 2004-12-30

FRIOR FILING DATE: 2003-12-30

NUMBER: OF SEQ ID NOS: 782

SOFTWARE: PALENTIN VERSION 3.3

SEQ ID NO 272

LENGTH: SA
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; ORGANISM: Eucalyptus sp.
US-11-024-959-272
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551.408 Million cell updates/sec
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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                                                                       OM protein - protein search, using sw model
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                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

N N	Description		Adw12903 Human SMA	Adw12907 Human SMA	_	Aaw15506 Mitogen a	Aam38754 Human pol	Abr43898 Human ERK		-		Adq37846 Human pho	Adv42070 Human ext		Adz65036 Mitogen a			Aag67618 Amino aci	Aag67439 Amino aci	_	Abu89742 Protein d	Abr62625 Human pro	Ado24425 Human PRO	Adz10062 Human bre		Aay70778 EGFP-Erkl
SUMMARIES	Ę		ADW12903	ADW12907	ABU54596	AAW15506	AAM38754	ABR43898	ADF45050	ADH59632	AD022522	ADQ37846	ADV42070	ADW12905	ADZ65036	AAM40540	AAY42413	AAG67618	AAG67439	ABG31847	ABU89742	ABR62625	AD024425	AD210062	AAW85006	AAY70778
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Aaw85015 Brkl-gree Abp96053 Human pro Aam48013 Extracell Adc6458 Human ext		Human Human Human Human	Human Human Human Human	AD743899 Human kin Adf49051 Human kin Adh59634 Brk2 prot Adj6608 ERK prote Adp56268 Human PRO
AAW85015 ABP96053 AAM48013 ADC64458	ADG98194 AAR20103 ABM82549 ABM82547	ADH48364 ABM82550 ABM82548 ADW12901	ADC64459 ADG98195 ABG31848 ABR92109	ABR43899 ADF45051 ADH59634 ADJ66608 ADP56268
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25 27 27 27 27	33033	333 354 36	33 39 40	4 4 4 4 4 11 2 E 4 2

## ALIGNMENTS

ADW12903 standard; protein; 359 AA.

RESULT 1 ADW12903

ADW12903;

New isolated SMAPK3 polypeptides and nucleic acids, useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal. The invention relates to novel isolated polypeptide (I) comprising an amino acid sequence selected from sequences comprising 335 or 359 amino acids (ADM12901 or ADM12903) or its fragments. The polypeptides and polynucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMARK3 gene in a mammal. The fragments of the polypeptides and polynucleotides can also be used as primers or probes. This sequence corresponds to the SMARX3VI variant DNA purification; diagnosis; cancer; mitogen-activated protein kinase; Claim 1; SEQ ID NO 4; 55pp; English. Human SMAPK3V2 variant protein. 18-JUL-2003; 2003US-00623108. 18-JUL-2003; 2003US-00623108. 07-APR-2005 (first entry) WPI; 2005-080923/09. N-PSDB; ADW12902 US2005013817-A1. (DAIK/) DAI K. Homo sapiens. 20-JAN-2005. protein enzyme. Dai K; 

Sequence 359 AA;

Sequence 359 AA;

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                                                                                                           VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                         KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                        NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel isolated polypeptide (I) comprising an amino acid sequence selected from sequences comprising 335 or 359 amino acids (ADM12901) or ADM12903) or its fragments. The polypeptides and polymucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SWAPK3 gene in a mammal. The fragments of the polypeptides and polymucleotides can also be used as primers or probes. This sequence corresponds to the SWAPK3V1 variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purification; diagnosis; cancer; mitogen-activated protein kinase;
                                                                      MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                             DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                         Gaps
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   Length 359;
                        Indels
; Score 1879; DB 9;
; Pred. No. 8.2e-187;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SMAPK3V4 variant protein.
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 359; Conservative 0
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                                                                                                                                                                                                                                                                    NRPIFPGKHYLDQLMHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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                                                                                                                                                                                                                                1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                       1 MAAAAAQGGGGGBPRRTEGVGPGVPGBVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                        DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                          Gaps
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                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiomyopathy; diabetes; ASD;
                          Indels
; Score 1879; DB 9;
; Pred. No. 8.2e-187;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; NOVX; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                    ABU54596 standard; protein; 359
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2001US-028136P.
2001US-028136P.
2001US-0281906P.
2001US-0282930P.
2001US-0282934P.
2001US-0282934P.
2001US-028234P.
2001US-028374P.
2001US-028374P.
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 100.0%;
100.0%;
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                             Conservative
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               Similarity
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05-APR-2001; 2
06-APR-2001; 2
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12-APR-2001;
13-APR-2001;
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20-APR-2001; 2
23-APR-2001; 2
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03-APR-2001;
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19-APR-2001;
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                           Matches 359;
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    Query Match
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                  Local
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cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic cardiomyopathy, diabetes, hypertension, congenital heart defects, actial septeal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, aubaortic stenosis, ventricular septeal defect (VSD), valve diseases, tuberous sclerosis, scleroderma atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABU54647 represent human NOVX polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;
Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgese CE, Gerlach V;
Padigaru M, Shimkete Rangoll EA, Taupier RJ, Casman SJ, Ji W;
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polypeptides, termed NOVX, and the polymucleotides encoding them. The polypeptides and polymucleotides are useful for diagnosing disease. The polympeptides are useful for potential therapeutic agents. The sequences are useful for treating metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 212; 666pp; English.
            24-APR-2001; 20010S-0286068P.
25-APR-2001; 20010S-0286292P.
27-APR-2001; 20010S-0286292P.
29-MAY-2001; 20010S-0294164P.
39-MAY-2001; 20010S-0294164P.
39-MAY-2001; 20010S-0294164P.
39-JUN-2001; 20010S-0299484P.
39-JUN-2001; 20010S-029927P.
39-JUN-2001; 20010S-029927P.
35-SEP-2001; 20010S-0318750P.
35-SEP-2001; 20010S-0324802P.
35-SEP-2001; 20010S-0324802P.
35-SEP-2001; 20010S-0324802P.
35-SEP-2001; 20010S-0324802P.
37-OCT-2001; 20010S-0330143P.
37-MOV-2001; 2001US-0332131P.
31-NOV-2001; 2001US-0332131P.
31-NOV-2001; 2001US-0332131P.
31-NOV-2001; 2001US-0332131P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
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N-PSDB; ABX72224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellerman K;
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95JP-00320577. 96EP-00104966 (TAKE ) TAKEDA CHEM IND LTD. Fani A, Ichimori Y; WPI; 1996-444623/45. Homo sapiens. 28-MAR-1996; 08-DEC-1995; EP735370-A1. 28-MAR-1995; 02-OCT-1996. 9 9 1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGBGAYGMVSSAY 1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY 0; Gaps Length 359; 1; Indels Score 1873; DB 6; Pred. No. 3.5e-186; 0; Mismatches 99.7**%**; 99.7**%**; Local Similarity ...

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241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                                 241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL 180
                                                                                                                                                                                                                                                                                                                                                               301 SKALDLIDRMLTFNPNKRITVABEPFTFAMELDDLPKERLKELIFQETARFQPGVLEAP 359
                                                                                                                                                                                                                                                                                                                                                                                                         301 SKALDLIDAMITFNPNKRITVAREPFTFAMELDDIPKERLKELIFQETARFQPGVLEAP 359
                                                                                                                KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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ઠે 셤 ò AAW15506 standard; peptide; 379 AA

AAW15506;

(first entry) 03-JUN-1997

Mitogen activating protein kinase ERK1.

Antibody; MAP kinase; human; mitogen activated protein; lymphoid cell; recognition sequence; IgG; immunogen; rat; ERK2; hybridoma; spleen cell; MAP kinase-related disease; cancer-associated disease; brain tumour; metabolic disorder; diabetes mellitus; circulatory disease; rheumatism; arteriosclerosis; allergic diseases; central nervous system disease; asthma; Alzheimer's disease; Parkinson's disease; senile dementia; ERK1; bone/joint disease; pollenosis; atopic dermatitis.

95JP-00070125.

95JP-00305456.

New antibodies to human MAP kinase - used for the detection, assay purification of various MAP kinase species.

Example 3; Page 34-35; 59pp; English.

This sequence represents the human mitogen activated protein (WAP) kinase ERKI. Fragments of this sequence (such as AAW15501) are recognition esquences for the antibodies of the invention. The antibodies of the invention. The antibodies of the invention. The antibodies of the invention are 1gG type monoclonal antibodies (WAD) generated by using the human ERKI as an immunogen and are capable of binding to BKRI at the Sites represented by these peptides. However, the MAD is incapable of binding to human or rat MAP kinase ERKI. The MAD are produced from cloned hybridomas derived from spleen cells of a mammal immunised with human erkil and homologous or heterologous lymphoid cells. The antibodies can be used for detecting or assaying MAP kinases. They can be used for diagnosing MAP kinase-related diseases, such as cancerassociated diseases (e.g. brain tumour), metabolic disorders (e.g. diabetes mellitus), circulatory disease (e.g. arteriosclerosis), allergic diseases (e.g. asthma, pollenosis, atopic dermatitis), central nervous system diseases (e.g. hlzheimer's disease, Parkinsonism, senile dementia) and bone/joint diseases (e.g. rheumatism). They can also be used to investigate the role of MAP kinases in-vivo and the mechanism of drug

DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120

61 61 121

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Query Match

Matches

VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKFSNLLINTTCDL 180

29-NOV-2000; 2000US-00727344,

us-10-623-108-4.rag

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action. The antibodies can also be used for purifying MAP kinases. By using antibodies specific for various types of MAP kinase, the activity of any given species of MAP kinase can be detected or assayed with high sensitivity to the exclusion of other species of MAP kinase
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                                                                                                                                                                                                                                                                                                  121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                                                                                                                                                                                                                                                                                                   NRPI FPGKHYLDQLNHILGILGSPSQEDLNCI INMKARNYLQSLPSKTKVAWAKLFPKSD
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                                                                                                                                                                                      MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                  DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                                                                                           VODLMETDLYKLLKSQQLSNDH1CYFLYQ1LRGLKY1HSANVLHRDLKPSNLLINTTCDL
                                                                                                                                Gaps
                                                                                                                              Indels 20;
                                                                                                  Length 379;
                                                                                                  Query Match 98.9%; Score 1859; DB 2; Best Local Similarity 94.7%; Pred. No. 1.1e-184; Matches 359; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SKALDLLDRMLTFNPNKRIT------
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25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
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03-AUG-2000; 2000US-00653450.
18-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
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                                                                        Sequence 379 AA;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in quene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous for a localised neuropathy and contral nervous system diseases, such as a lateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and therapy, drug screening, assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation. leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form the printed specification
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Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                              nucleic acids and polypeptides, useful for treating disorders such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINWKARNYLQSLFSKTKVAWAKLFPKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAAAAAQGGGGGFPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                       Ren F, Wa
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                      Qian XB,
Yang Y,
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Pred. No. 1.1e-184;
0; Mismatches 0;
                                                       , Ma Y, (
Xue AJ,
                                                                                                                                                                                                           Example 3; SEQ ID NO 1899; 10078pp; English.
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                                                       Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                             central nervous system injuries.
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Matches 359; Conservative
                                                                                                                    WPI; 2001-442253/47.
                             (HYSE-) HYSEO INC
                                                                                                                                   N-PSDB; AAI57910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 379 AA;
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                                                       Tang YT,
Wang J,
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Zhou P,
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AC ABR4
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              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying an agent to be tested for ability to treat psychotic disorder in patient. The method involves contacting cells of tissues with a candidate drug, and determining levels of phosphorylation of intracellular signaling proteins DARPP-32 (dopamine-and cAMP-regulated phosphoprotein), ERK1 and ERK2 (extracellular signal-regulated protein kinases 1 and 2), and CREB (CAMP-response element binding protein). The method is useful for identifying an agent to be tested for an ability to treat a psychotic disorder such as schizophrenia in a patient in need of such treatment. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying agent to be tested for ability to treat psychotic disorder, by contacting cells/tissues with candidate drug, determining phosphorylation levels of intracellular signaling proteins DARPP-32, ERK1, ERK2, CREB.
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                                                             DARPP-32; psychotic disorder; intracellular signaling protein; dopamine- and cAMP-regulated phosphoprotein; BRKI; BRKZ; CRBB; extracellular signal-regulated protein kinase; phosphorylation; cAMP-response element binding protein; schizophrenia; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1859; DB 6; Length 379;
Pred. No. 1.1e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 77-78; 79pp; English.
                                                                                                                                                                                                                                                                                     31-AUG-2001; 2001US-0316338P.
                                                                                                                                                                                                                                                    03-SEP-2002; 2002WO-US027802
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(first entry)
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                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
(KARO-) KAROLINSKA INST.
                                                                                                                                                                                                                                                                                                                                                                          Greengard P, Fisone G;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-300912/29
                                 Human ERK1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human ERK1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 379 AA;
                                                                                                                                                                                   WO2003021225-A2.
11-AUG-2003
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                   13-MAR-2003
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The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
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Pred. No. 1.1e-184;
0; Mismatches 0; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; protein kinase; enzyme; inhibitor; ERK1.
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                                         361 KELIFQETARFQPGVLEAP 379
                                                                                                                                                                                           ADF45050 standard; protein; 379
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Best Local Similarity 94.7%;
Matches 359; Conservative (
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                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     Human kinase ERK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
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                                                                                                 1 MAAAAAQGGGGGBPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                    DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                              VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                                                                                                                                                                                                                                       KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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                                                           1 MAAAAAQGGGGGPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                   DHVRKTRVAIKKISPPEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biochemical pathway; mammalian glioma tumour;
epidermal growth factor receptor; EGFR; mTOR; polypeptide inhibitor;
cancer; ERK; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of biochemical pathways associated with glioblastoma for, e.g. identifying a mammalian glioma tumor that is likely to respond to epidermal growth factor receptor polypeptide inhibitor or an mTOR polypeptide inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemical pathway-related human ERK protein SeqID8
   No. 1.1e-184;
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   Pred. No. 1.16
0; Mismatches
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(CELL-) CELL SIGNALING TECHNOLOGY INC.
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94.78;
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                     359; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-411736/38.
   Similarity
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 Best Local &
Matches 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying and/or obtaining a compound useful for preventing or treating cardiac diseases, particularly congestive heart failure, comprises quantification of the activity of Raf-1, MEK1/2 and/or Erk1/2 depending
                         300
                                             241 NRPIFPGKHYLDQLNHIIGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                   340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac disease; Raf-1; MEX1; Cardiant; telethonin; &agr-actinin; hypertrophy; MEK2; Erk1; Erk2.
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                                                                                                                                                                                                                                                                                                               ADH59632 standard; protein; 379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leclair S,
                                                                                                                                                                                                    361 KELIFQETARFQPGVLEAP 379
                                                                                                                                                                              KELIFQETARFQPGVLEAP 359
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24-SEP-2001; 2001US-0324625P
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                                                                                                                                                                                                                                                                                                                                                                                                                                Erkl protein
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'n Henkel Nave

This invention relates to a novel use of biochemical pathways for identifying a mammalian glioma tumour that is likely to respond to an epidermal growth factor receptor (EGFR) polypeptide inhibitor or an mTOR Claim 1; SEQ ID NO 8; 66pp; English.

98.9%; Score 1859; DB 7; Length 379;

Sequence 379 AA;

Query Match

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       tumour that does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; HER-2 directed therapy; tumour; insulin growth factor receptor; IGFR; epidermal growth factor receptor; EGFR; S6 ribosomal protein; AKT; NDF; ERK; cancer therapy; predictive biomarker; HER-2/neu.
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                                                                                                                                                                                                                              9
polypeptide inhibitor, or identifying a mammalian glioma tumour that do not expresse a PTEN polypeptide and which is likely to respond or not likely to respond to an inhibitor of mTOR polypeptide activity, respectively. The biochemical pathways are, in particular, disregulated in pathologies sa cancer. The present sequence is that of the human ERK protein which may be used in the method of the invention.
                                                                                                                                                                                                                                                                            DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLBAMRDVYI
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                                                                                                                                                                                                                   1 MAAAAQGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQXIGEGAYGMVSSAY
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                                                                                                                                                                                                   MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                         Gaps
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                                                                                                                                                                         20;
                                                                                                                                            Length 379;
                                                                                                                                                                        0; Indels
                                                                                                                                             Score 1859; DB 8;
Pred. No. 1.1e-184;
                                                                                                                                                                         0; Mismatches
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                                                                                                                                             Query Match
Best Local Similarity 94.7%;
Matches 359; Conservative
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at 202
                                                                                                                    Sequence 379 AA;
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This invention relates to a novel method for determining or predicting the response of a patient to HER-2 directed therapy. Specifically, it refers to analysing a mammalian tumour in order to detect a pattern of expression and/ or phosphorylation of a protein taken from the group including insulin growth factor receptor (IGFR) polypeptide, epidermal growth factor receptor (IGFR) polypeptide, epidermal phosphorylated AKT, phosphorylated NDF or phosphorylated ERK protein. The present invention describes characterising a mammalian tumour's responsiveness to an HER-2 therapy and hence an individual's response to this cancer therapy, using an immunologically specific antibody directed against one of the aforementioned proteins. Furthermore, it provides predictive biomarkers that can be used to assess the efficacy of the human phosphorylated ERK protein of the invention.
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                                                                                                                            Identifying a mammalian tumor, useful for predicting a response to HER2-directed therapy, comprises assaying a sample to detect a pattern of expression, phosphorylation or both, of one or more polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1859; DB 8;
Pred. No. 1.1e-184;
0; Mismatches 0;
                             (VENT-) VENTANA MEDICAL SYSTEMS INC. (CELL-) CELL SIGNALING TECHNOLOGY INC.
                                                                                                                                                                                         Claim 35; SEQ ID NO 3; 49pp; English
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11-DEC-2002; 2002US-0432942P.
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Best Local Similarity 94.7
Matches 359; Conservative
                                                                                                     WPI; 2004-507069/48
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 379 AA;
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KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS

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240 240 360

KELIFQETARFOPGVLEAP 359 KELIFQETARFQPGVLEAP 379

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361

SKALDLIDRMLTFNPNKRIT-------VAEEPFTFAMELDDLPKERL

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The invention relates to a novel method for identifying a mammalian tumor responding to HER2-directed therapy, where the tumor overexpresses HER2. The method involves assaying a sample obtained from the mammalian tumor to detect a pattern of expression and/or phosphorylation of one or several polypeptides chosen from inaulin-like growth factor receptor (IGFN) polypeptide, neu (IGFN) polypeptide, neu cipentiation factor (NDF) polypeptide, phosphorylated S6 ribosomal polypeptide, phosphorylated AKT polypeptide, where the polypeptide, phosphorylated AKT polypeptide and phosphorylated control regular regulared kinase (ERK) polypeptide, where the cetected pattern of expression, phosphorylation or both expression and phosphorylation identifies mammalian tumors that respond to HER2-directed therapy. The method of the invention is useful for identifying a mammalian tumor that responds to a HER2-directed therapy, or does not respond to HER2-directed therapy.

The invention is useful for identifying a mammalian tumor that responds to a HER2-directed therapy, or does not respond to HER2-directed therapy.

The argeting HER2 or subject with cancer for treatment with a molecule targeting HER2. The method is useful for determining or predicting response to HER2-directed therapy in an individual. The method enables predicting response to HER2-directed therapy in an individual. The method canables prediction of response in cancer subjects to cancer therapy. The method of present sequence represents the numan ERK protein used in the method of present sequence represents the numan ERK protein used in the method of prediction of response in cancer subjects in the method of prediction of response in cancer subjects in the method of prediction of response in cancer subjects in the method of prediction of response in cancer subjects in the method of prediction of response in cancer subjects in the method of the prediction of response in cancer subjects in the method of the prediction of the prediction of the prediction of the predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying mammalian tumor responding to HER2-directed therapy, involves assaying sample from tumor to detect expression and/or phosphorylation of insulin-like growth factor receptor polypeptide/erb81 receptor
                                                tumor, antibody therapy; human epidermal growth factor receptor 2; HER2; phosphorylation; extracellular signal regulated kinase; ERK.
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Human extracellular signal regulated kinase SEQ ID NO:3.
                                                                                                                                                                                                                                     note= "phosphorylated"
                                                                                                                                                                                                                                                                                      /note= "phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENTANA MEDICAL SYSTEMS INC.
                                                                                                                                                                                  Location/Qualifiers
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11-DEC-2002; 2002US-0432942P.
07-APR-2003; 2003US-00408520.
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2003; 2003US-00735118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith BL;
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                                                                                                                                                                                     Key
Modified-site
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                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                         New isolated SMAPK3 polypeptides and nucleic acids, useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal.
                                                                                                               purification; diagnosis; cancer; mitogen-activated protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel isolated polypeptide (I) comprising an amino acid sequence selected from sequences comprising 335 or 359 amin acids (ADW12901 or ADW12903) or its fragments. The polypeptides and polynucleotides are useful for diagnosing diseases, e.g. cancers, associated with the deficiency of the SMAPK3 gene in a mammal. The fragments of the polypeptides and polynucleotides can also be used as primers or probes. This sequence corresponds to the SMAPK3VI variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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94.7%; Pred. No. 1.1e-184;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6; 55pp; English.
ADW12905 standard; protein; 379 AA.
                                                                                   Human SMAPK3V3 variant protein.
                                                                                                                                                                                                                                                18-JUL-2003; 2003US-00623108
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                                                        (first entry)
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Matches 359; Conservative
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N-PSDB; ADW12904.
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protein.
                                                                                                                                                                                        US2005013817-A1.
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                                                                                                                                                                                                                                                                                                       (DAIK/) DAI K.
                                                                                                                                                              Homo sapiens.
                                                        07-APR-2005
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                           ADW12905;
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DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120 DHVRKIRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120

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Gaps

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1 MAAAAAQGGGGGBPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY MAAAAAQGGGGGEPRKTEGVGPGVPGEVEMVKGQPPDVGPRYTQLQYTGEGAYGMVSSAY

Matches 359; Conservative

Local Similarity

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9 9 120 120 180 180 240 240 300 300 340

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cancer
                                                         Indels
constitutive expression of P-MAPK is indicative of
                                      Score 1859; DB 9;
Pred. No. 1.1e-184;
                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 5471.
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2000US-00488725.
2000US-00552317.
2000US-00520312.
2000US-00653450.
2000US-00653450.
2000US-00653450.
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                                     Query Match
Best Local Similarity 94.7%;
Matches 359; Conservative
                    Sequence 379 AA;
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25-APR-2000;
20-JUN-2000;
19-JUL-2000;
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14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting phosphorylated mitogen activated protein kinase (P-MAPK), by contacting sample with antibody having affinity for P-MAPK, detecting antibody/P-MAPK complex to detect P-MAPK, and expression of P-MAPK
                                                                                          VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                                                                                  KICDFGLARIADPEHDHTGFLTEYVATRWYRAPBIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                        NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
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                                                                                                                                                                                                    SKALDLLDRMLTFNPNKRIT-------VAEEPFTFAMELDDLPKERL
                                                                                                                     KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
   MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
              VQDIMETDLYKLIKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
                                                                                                                                                                                                                                                                                                                                                                                           MAP kinase; Mitogen-activated protein kinase; enzyme; cancer.
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                                                                                                                                                                                                                                                                                                                standard; protein; 379
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14-OCT-2003; 2003WO-US032248.
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARBI/) ARBISER J L. (COHE/) COHEN C.
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REFSEQ; XP_055766.3.
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181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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                                                                                                                                                                                                                                                                                          61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLKRRHENVIGIRDILRASTLEAMRDVYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
                                                                                                                                                                  61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                              1 MAAAAAQGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                  20;
Length 379
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous as system, such as localised neuropathies and central nervous system disease, such as lazhemer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                Ren F, Wang D;
Zhang J, Zhao QA;
                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
              Liu C, Asundi V, Chen R, Ma Y, Qian XB, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 5471; 10078pp; English.
                                                                                                              2001-442253/47
                                                                                                                                    N-PSDB, AAI59696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 403 AA;
                                          , u,
                       Tang
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120 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180 145 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 204 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240 205 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 264 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300 -----VAEBPFTFAMELDDLPKERL 340 84 25 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVENVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY Gaps 20; Length 403; Indels Score 1859; DB 4; Pred. No. 1.2e-184; 0; Mismatches 0; SKALDLLDRMLTFNPNKRIT---vuery match 98.9%; Best Local Similarity 94.7%; Matches 359; Conservative 0 265 301 61 85 121 181 241 325 g q 엄 ઠ 8 엄 ò d ઠે ò g ò

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Best Local Similarity 94.5
Matches 358; Conservative
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Query Match
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                                                                                                                               AAY42413 standard; protein; 379 AA
                                                               KELIFQETARFQPGVLEAP 359
                                                                                 403
                                                                           KELIFQETARFOPGVLEAP
                                                                                                                                                                 (first entry)
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341 385 Extracellular signal Regulated Kinase (ERK)1 mutant.

02-DEC-1999

AAY42413;

RESULT 15
AAY42413
ID AAY42
XX
AC AAY42
XX
DT 02-DE
XX
XX
DE EXTRA

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This is the amino acid sequence of ERKI. Substitution of glutamine with an amino acid with a small side chain, such as alanine and threonine foresteate a mutant kinase which can theoretically bind to a pyridinylimidazole inhibitor of p38. (Map) 1 kinase. Map 1 kinases mediate intracellular signal transduction pathways and so have a role in many diverse human diseases. For example, kinases have been implicated in cell nearty into apoptosis, cancer, Alzheimer's disease, angiotensin II and hematopoietic cytokine receptor signal transduction, oncoprotein signalling and mitosis, inflammation and infection, etc. Members of the Map kinase family share sequence similarity and conserved structural domains, and include the extracellular-signal regulated kinases (ERKS), Jun N-terminal kinases (JNKS) and p38 kinases. The invention relates to methods for designing inhibitors of serine/threonine kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VQDIMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method of designing Ser/Thr or Tyr kinase inhibitor useful for treating, example breast cancer, restenosis, asthma or hypertension.
                mitogen activated protein; MAP kinase; apoptosis; cancer; inflammation;
                                                                                                                                                                          /note= "Glu can be substituted by an amino acid with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly MAP kinases, and tyrosine kinases through the use of ATP-binding site mutants of these kinases. The methods of this invention tradvantage of the fact that the mutant kinases are capable of binding inhibitory compounds of other kinases with greater affinity than the corresponding wild-type kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                intracellular signal transduction pathway; inhibitor; wildtype; ERK; extracellular signal regulated kinase; pyridinyl-imidazole.
                                                                                                                                                                                               small side chain, for example alanine or threonine"
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Pred. No. 4.6e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.6%; bcc...
94.5%; Pred. No. *...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Germann UA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 50-51; 71pp; English.
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       99WO-US003181.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson KP,
                                                                                                                                                                                                                                                                                                                                                                                                 (VERT-) VERTEX PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-540310/45.
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                                                                                                                                          Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                       16-FEB-1999;
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                        WO9942592-A1
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8
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241 NRPIFFGKHYLDQLMHILGILGSPSQEDLMCIINMKARNYLQSLPSKTKVAWAKLPPKSD 300
         8 6 8 6 8
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Search completed: February 6, 2006, 15:29:02 Job time : 287.562 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                     Copyright
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OM protein - protein search, using sw model

February Run on:

6, 2006, 15:29:28; Search time 26.8991 Seconds (without alignments) 1284.124 Million cell updates/sec

US-10-623-108-4 1879 1 MAAAAAQGGGEPRRTEGV......LKELIFQETARFQPGVLEAP 359 Perfect score:

Sequence:

Scoring table:

283416 segs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 80:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	MAP kinase 3 (EC 2	Ca2+/calmodulin-de	Ca2+/calmodulin-de	Ca2+/calmodulin-de	extracellular sign	MAP kinase 1 (EC 2	protein kinase ERK	mitogen-activated	protein kinase (EC	mitogen-activated		extracellular sign	MAP kinase mpk-1 (	MAP kinase sur-1 (	pathogenicity MAP	mitogen-activated	protein kinase (EC	mitogen-activated	protein kinase ERK	mitogen-activated	mitogen-activated		protein T30E16.13	mitogen-activated	mitogen-activated	mitogen-activated	mitogen-activated,	mitogen-activated	extracellular sign
SUMMARIES	ΩI	A48082	JC1451	S28184	A60041	JW0052	JQ1400	S25011	S16444	A40033	A39754	JW0053	A46036	A36978	A36977	T51944	T51943	S15663	A56042	A47211	S48123	833635	\$51320	F96619	S40472	851321	839559	S52989	S40470	B56708
	DB	-	1 (2)	7	7	~	Н	N	7	~	7	~	~	N	~	7	~	7	~	7	7	7	~	N	~	~	~	N	0	7
	* Query Match Length	379	380	377	369	392	360	360	358	358	361	369	376	376	444	356	361	372	415	362	387	394	371	376	395	393	372	384	376	815
	* Query Match	98.6	94.9	94.9	94.0	82.5	81.9	81.9	81.3	81.3	80.7	80.3	72.6	70.1	70.1	49.6	48.9	47.0	46.0	45.7	44.6	44.0	44.0	43.7	43.7	•	43.3	•	43.3	43.0
	Score	1853	1784	1783	1767	1550.5	1538.5	1538.5	1528.5	1528.5	1516	1508	1364.5	1317	1317	932	918.5	884	865	859.5	837.5	827	826.5	822	822	817	814	814	-	807.5
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356 2 S56638 370 2 S40469 368 2 A33297 368 2 CA32297 353 2 S28548 373 2 P6236 376 2 S40471 375 2 T03971 376 2 S40471 371 2 T09622 371 2 T09622 371 2 T14915 369 2 C86146	mitogen-activated	mitogen-activated	mitogen-activated	probable serine/th	hypothetical prote	protein kinase (EC	mitogen-activated	protein F14N23.9 [	mitogen-activated	mitogen-activated	mitogen-activated	mitogen-activated	protein kinase MMK	MAP kinase (ATMPK7	mitogen-activated	hypothetical prote	
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## ALIGNMENTS

Nicontains: protein kinase (EC 2.7.1.37)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 04-Sep-1998 #sequence revision 04-Sep-1998 #text_change 09-Jul-2004
Cipate: 04-Sep-1998 #sequence revision 04-Sep-1998 #text_change 09-Jul-2004
Cipates Procession: A46082; PQ0270; S23428; S15519; S21579
R;Charest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.
A;Cibatest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.
A;Title: Molecular cloning, expression, and characterization of the human mitogen-activat A;Reference number: A48082; MUID:93330262; PMID:7687743

A; Status: translation not shown A; Molecule type: mRNA A; Accession: A48082

A; Residues: 1-379 «CHA»
A; Residues: 1-379 «CHA»
A; Cross-references: UNIPROT: P27361; UNIPARC: UP10000035BE2; EMBL: X60188; NID: 931220; PIDN
A; Cross-references: UNIPROT: P27361; UNIPARC: UP10000035BE2; EMBL: X60188; NID: 931220; PIDN
A; Cross-references: UNIPROT: P27361; UNIPARC: UP10000035BE2; EMBL: X60188; NID: 931220; PIDN
B; Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.
Biochem. Biophys Res. Commun. 182, 1416-1422, 1992
A; Title: Extracellular signal-regulated kinases in T cells: characterization of human ERP
A; Reference number: JQ1400; MUID: 92171961; PMID: 1540184

A;Reference number: S23426; MID:9216223; PIDN:AAA36142.1; PID:c. A;Experimental source: cell line CEM
R;Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
FEBS Lett. 304, 170-178, 1992
A;Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.
A;Reference number: S23426; MUID:92316223; PMID:1319925 A; Molecule type: mRNA

A;Molecule type: mRNA A;Residues: 25-13,1',175-379 cGON> A;Cross-references: UNIRARC:UPIO00016A2B4; EMBL:Z11696; NID:923882; PIDN:CAA77754.1; PID C;Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723). A;Accession: S23428

AjGene: GDB:PRKM3; ERK1 AjCross-references: GDB:135679; OMIM:601795 AjMap position: 16pter-16qter Cj.Complex: monomer

C; Function:

A.Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A.Pathway: MAP kinase cascade
A.Pathway: MAP kinase calated transforming protein; protein kinase homology
C.Superfamily: kinase-ralated transforming protein; phosphotransferase; serine/threonine-specific [F;40-330/Domain: protein kinase homology «KIN»
F;48-56/Region: protein kinase homology «KIN»
F;202/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted F;204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted

2

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14-94,'R',96-380 <DEM>
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GG24/Callmodulin-dependent protein kinase (BC 2.7.1.123) - rat
GG24/Callmodulin-dependent protein kinase; extracellular signal-regulated kinase
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Dacession: JG2451; A35061; A37140; A40466; S24947
C.Accession: JG2451; A35061; A37140; A40466; S24947
R.Marquard, B.; Stabol, S.
GGRID, SQUADENCE Of a rat cDNA encoding the ERK1-MAP kinase.
A.Rocession: JG1451; MUD:33013050; PMID:1327976
A.Rocession: JG1451; MUD:33013050; PMID:1327976
A.Rocession: JG1451; MUD:33013050; PMID:1327976
A.Rocession: JG1451; MUD:3013050; PMID:1327976
A.Rocession: JG1451; MUD:3013050; PMID:13147; EMEL:K65198; NID:25626; PIDN
A.Recidues; 1.380 cMAPA
A.Rocession: A5061; MUD:901312137; PMID:2164259
A.Accession: A35061
A.Rocession: A3140
A.Rocession: A3046
A.Rocession: A3040
A.Rocession
                                                                                                                                                                                        DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                   VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL 180
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                                                                                                                           1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                 Gaps
                                                 20;
Length 379;
                                                 Indels
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  Score 1853; DB 1;
Pred. No. 1.1e-77;
                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKALDLLDRMLTFNPNKRIT
  Query Match
Best Local Similarity 94.5%;
Matches 358; Conservative
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A;Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:g515498; PIDN:AAA200 C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; calmodulin binding; phosphortein; phosphotransferase; serine/threonine F;41-331/Domain: protein kinase homology KKIN:
F;49-57/Region: protein kinase ATP-binding motif
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A;Residues: 7-16 <CRE>
A;Cross-references: UNIPARC:UPIO000170C57; GB:S58470; NID:9236372; PIDN:AAB19973.1; PID:
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming protein; protein kinase
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A;Molecule type: mRNA
A;Rossidues: 1-377 <TAN>
A;Cross-references: UNIPROT:Q63844; UNIPARC:UPI000017558C; EMBL:Z14249
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
NA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse A;Reference number: A40466; MUID:91369479; PMID:1716439
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() Species: Mus musculus (house mouse)
() Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
() Accession: S28184; B40466; Ā41371
() Attaner, B.; Mueckler, M.
Biochim. Biophys. Acta 1171, 319-320, 1993
A;Title: Molecular cloning of a mouse extracellular signal regulated kinase (erk-1).
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A,Molecule type: mRNA
A,Reaidues: 74-377 < CEM
A,Reaidues: 74-377 < CEM
A,Cross-references: UNIPARC: UPI0000023599; GB:S59517
R,Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.
Proc. Natl. AAcad. Sci. U.S.A. 88, 8845-8849; 1991
A,Fitle: Mouse Erk 1 gene product is a serine/threonine protein kinase that has the 1
A,Reference number: A41371; MUID:92020947; PMID:1717989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLK 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 KALDLIDRMLTFNPNKRITVEBALAHPYLEQYYDPTDEPVAEBPFTFDMELDDLPKERLK 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSN
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                                                                                                                                                                                                                       94.9%; Score 1784; DB 2; Length 380; 91.8%; Pred. No. 1.5e-74;
                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                 1; Mismatches
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Matches 347; Conservative
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extracellular signal-regulated kinase (BC 2.7.-.-) 1 - common carp)
NyAlternate names: CBRK1
C;Species: Cyprinus carpio (common carp)
C;Species: Cyprinus carpio (common carp)
C;Species: Cyprinus carpio (common carp)
C;Accession: JW0052
R;Hashimoto, H.; Yokoyama, Y.; Matsuo, Y.; Toyohara, H.; Kohno, M.; Sakaguchi, M.
J. Biochem. 123, 1031-1035, 1998
A;Title: Existence of two isoforms of extracellular signal-regulated kinase in fish.
A;Reference number: JW0052; MUID:98269030; PMID:9603989
A;Accession: JW0052
A;Reference number: JW0052; MUID:98269030; PMID:9603989
A;Cross-references: UNIPROT:Q7LZH4; UNIPARC:UPI0000175598
A;Cross-references: UNIPROT:Q7LZH4; UNIPARC:UPI0000175598
C;Comment: This enzyme is the key enzyme in the intracellular signal transduction pathwas C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: Phosphotranaferase
F;54-344/Domain: protein kinase homology <KIN>
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                                                                                                        LDQLMHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRM
                                      ADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHY
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82.5%; Score 1550.5; DB 2; Length
Best Local Similarity 78.5%; Pred. No. 5.8e-64;
Matches 300; Conservative 20; Mismatches 29; Indels
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Action 1
Ca2+/calmodulin-dependent protein kinase (BC 2.7.1.123) ERK1 - Chinese hamster (fragment Ca2+/calmodulin-dependent protein kinase (BC 2.7.1.123) ERK1 - Chinese hamster (Ca2+/calmodulin-dependent griseus (Chinese hamster)
C; Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C; Date: 06-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C; Date: 06-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C; Date: 06-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
R; Meloche, S.; Pages, G.; Pouyssegur, J.
Mol. Biol. Cell 3, 63-71, 1992
A; Title: Functional expression and growth factor activation of an epitope-tagged p44 mit
A; Reference number: A60041; MUID:92199340; PMID:1372523
A; Reference number: A60041; MUID:92199340; PMID:1372523
A; Residues: nct compared with conceptual translation
A; Residues: nct compared with conceptual translation
A; Residues: 1-369 - MEL
A; Cross-references: UNIPROT:Q7M0H9; UNIPARC:UPI000017558E
C; Comment: This serine/threonine kinase is activated in response to extracellular stimul
C; Superifamily: kinase-related transforming protein; protein kinase homology <a href="https://dx.nc./ciam/kinase-related-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relation-relati
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                                                                 Length 377;
                                                                                                               Indels
                                                                                         Pred. No. 1.6e-74;
1; Mismatches 10;
                                                                   DB 2;
F;38-328/Domain: protein kinase homology <KIN>F;46-54/Region: protein kinase ATP-binding motif
                                                                   Score 1783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALDLLDRMLTFNPNKRIT----
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91.8%;
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A/ACCESBION: 253420
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A/ACCESBION: S23420
A/ACCESBION: S23427
A/ACCESBION: S24230
A/ACCESBION: S24310
C/ACCESBION: S24310
A/ACCESBION: SAME ACCESBION: ACCESBION: A/ACCESBION: A/ACCESBION:
MAP kinase 1 (EC 2.7.1.-) - human MAP kinase 2 (ERKZ); mitogen-activate M.Alternate names: ERK; extracellular signal-regulated kinase 2 (ERKZ); mitogen-activate Ni, Alternate names: ERK; extracellular signal-regulated kinase (EC 2.7.1.37)
Ni, Alternate names: ERK; extracellular (EC 2.7.1.37)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: J01400; S23426; $23427; $21577; $21578
R; Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.
R; Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.
A; Title: Extracellular signal-regulated kinases in T cells: characterization of human ERA; Reference number: J01400; MUID:92171961; PMID:1540184
                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-360 <0WA>
A;Residues: 1-360 <0WA>
A;COSS-references: UNIPROT:P28482; UNIPARC:UPI00000104F; GB:M84489; NID:g182190; PIDN:A;Cross-references: cell line Jurkat
A;Experimental source: cell line Jurkat
R;Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
PEBS Lett. 304, 170-178, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Heterogeneous expression of four MAP kinase isoforms in human tissues A,Reference number: $23426; MUID:92316223; PMID:1319925
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Best Local Similarity 79.1¶
Matches 296; Conservative
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protein kinase ERKZ (EC 2.7.1.-) - bovine
N.Alternate names: extracellular signal-regulated kinase
C.Species: Bos primigenius taurus (cattle)
R.E.I., Cox. M.E.; Her, J.; Parsons, S.J.
Submitted to the EMBL Data Library, July 1992
A.Description: Cloning and sequencing of ERKZ from a bovine adrenal medula cDNA library.
A.Description: S25011
A.Status: preliminary
A.Scession: S2501
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: Date and Sequencing of ERKZ from a bovine adrenal medula cDNA library.
A.Status: preliminary
A.Stat
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Best Local Similarity 79.13
Matches 296; Conservative
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mitogen-activated protein kinase (EC 2.7.1.-) - mouse
NyAlternate names: cell division cycle-2-related protein kinase ERKZ
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: 816444; 815015; FN0480
R;Her, J.H.; Wu, J.; Rall, T.B.; Sturgill, T.W.; Weber, M.J.
Nucleic Acids Res. 19, 3743, 1991
A;Title: Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by A;Reference number: 816444; MUID:91305126; PMID:1649458

phá

tyrosine

A;Molecule type: mRNA A;Residues: 1.358 VHER> A;Crosa-references: UNIPROT:P27703; UNIPARC:UPI0000003FEA; EMBL:X58712; NID:953001; PIDN: A;Note: part of this sequence was confirmed by protein sequencing

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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-361 <POS>
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A; Residues: 1-4,'G',6
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                 EMBO J. 10, 885-892, 1991

A, Title: Identification of the regulatory phosphorylation sites in pp42/mitogen-activate
A, Reference number: S15015; MUID:91184134; PMID:1849075
A, Accession: S15015; MUID:91184134; PMID:1849075
A, Accession: S15015; MUID:91184134; PMID:1849075
A, Status: preliminary
A, Molecule type: protein
A, Residues: 171-181, XX, 183-189 < PAY>
A, Cross-references: UNIPARC:UPI0000175588
R, Ershler; M.A.; Nagorskaya, T.V.; Visser, J.W.M.; Belyavsky, A.V.
Gene 124, 305-306, 1993
A, Fitle: Novel CDC2-related protein kinases produced in murine hematopoietic stem cells.
A, Reference number: PN0479; MUID:93185941; PMID:8444355
A, Accession: PN0480
A, Status: nucleic acid sequence not shown
A, Molecule type: mRNA
A, Residues: 145-195 < CERS>
A, Access-references: UNIPARC:UPI0000175589
C, Superfamily: kinase-related transforming protein; phosphotransferase; serine/threonin
C, Keywords: ATP; cell cycle control; phosphoprocein; phosphotransferase; serine/threonin
F; 29-37/Region: protein kinase ATP-binding motif
F; 183/Binding site: phosphate (Tyr) (covalent) #status experimental
F; 185/Binding site: phosphate (Tyr) (covalent) #status experimental
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protein kinase (EC 2.7.1.37) ERK2 - rat
protein kinase (EC 2.7.1.37) ERK2 - rat
c;Species attus morvegicus (Norway rat)
C;Date: 21-Reb-1992 #sequence_revision 21-Peb-1992 #text_change 09-Jul-2004
C;Date: 21-Reb-1992 #sequence_revision 21-Peb-1992 #text_change 09-Jul-2004
C;Accession: A40033
R;Boulton, T.G; Nye, S.H.; Robbins, D.J.; Ip, N.Y.; Radziejewska, E.; Morgenbesser, S.D.
Cell 65, 663-675, 1991
A;Title: ERKs: a family of protein-serine/threonine kinases that are activated and tyros
A;Title: ERKs: a family of protein-serine/threonine kinases that are activated and tyros
A;Reference number: A40033
A;Status: preliminary
A;Status: preliminary
A;Residues: mRNA
A;Residues: 1-358 «BOU>
A;Cross-references: UNIPROT:P27703; UNIPARC:UPI0000003FEA; GB:M64300; NID:g204055; PIDN:
ŗ.
  D.M.; Rossomando, A.J.; Martino, P.; Erickson, A.K.; Her, J.H.; Shabanowitz,
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78.6%; Pred. No. 5.4e-63;
tive 19; Mismatches 22; Indels
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C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki P;21-311/Domain: protein kinase homology <KIN> F;29-37/Region: protein kinase ATP-binding motif
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C;Species: Xanopus laevis (African clawed frog)
C;Date: 07-Peb-1992 #sequence_revision 07-Peb-1992 #text_change 09-Jul-2004
C;Accession: A39754; S16597
R;Posada, J; Sanghera, J; Pelech, S.; Aebersold, R.; Cooper, J.A.
Mol. Cell. Biol. 11, 2517-2528, 1991
A;Pitle: Tyrosine phosphorylation and activation of homologous protein kinases during ook
A;Reference number: A39754; MUID:91203872; PMID:1708093
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A;Cross-references: UNIPARC:UP1000017156A; EMBL:X59813; NID:g64893; PIDN:CAA42482.1; PID
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Seywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k:
F;26-316/Domain: protein kinase homology <KIN.
F;34-42/Region: protein kinase ATP-binding motif
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R;Gotoh, Y.; Moriyama, K.; Matsuda, S.; Okumura, B.; Kishimoto, T.; Kawasaki, H.;
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A;Title: Xenopus M phase MAP kinase: isolation of its cDNA and activation by MPF A;Reference number: S16597; MUID:91330892; PMID:1714387
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                                                                                                                                                     DB 2; Length 358;
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77.8%; Pred. No. 2e-62;
iive 20; Mismatches 29;
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342 KELIFEETARFQPG 355
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Best Local Similarity 77.8%
Matches 291; Conservative
                                                                                                                                                     Query Match
Best Local Similarity 78.6'
Matches 294; Conservative
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1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY

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us-10-623-108-4.rpr

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C, Accession: A46036
R, Biggs III, W.H.; Zipursky, S.L.
Procession: A46036
R, Biggs III, W.H.; Zipursky, S.L.
Procession: A22. U.S.A. 89, 6295-6299, 1992
A, Title: Primary structure, expression, and signal-dependent tyrosine phosphorylation of A; Reference number: A46036; MUID:92335284; PMID:1378625
A, Recession: A46036
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1.376
A, Cross-references: UNIPROT:P40417; UNIPARC:UPI0000000FB3; GB:M95124; NID:g485754; PIDN:1
A, Cross-references: UNIPROT:P40417; UNIPARC:UPI0000000FB3; GB:M95124; NID:g485754; PIDN:1
A, Cross-references: FlyBase:FBgn0003256
C, Genetics:
A, Gene: FlyBase:I A, Cross-references: FlyBase:FBgn0003256
C, Seuperfamily: kinase-related transforming protein; protein kinase homology
C, Superfamily: protein kinase homology < KIN>
F; 34-52/Region: protein kinase ATP-binding motif
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MAP kinase mpk-1 (EC 2.7.1.-) - Caenorhabditis elegans
G.Species: Caenorhabditis elegans
C.Species: Caenorhabditis
R.Jackner, M.R.; Kornfeld, K.; Miller, L.M.; Horvitz, H.R.; Kim, S.K.
R.Jackner, M.R.; Kornfeld, K.; Miller, L.M.; Horvitz, H.R.; Kim, S.K.
A;Tille: A MAP kinase homolog, mpk-1, is involved in ras-mediated induction caenorhaber: A36978; MUID:94131270; PMID:8299936
A;Status: preliminary
                                                                                                                                                                                                                                                           extracellular signal-regulated kinase (EC 2.7.1.-) DmERK-A - fruit fly (Dro C;Species: Drosophila melanogaster
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
19 VPQSNAEVIRGQIFEVGPRYIKLAYIGEGAYGMVVSADDTLTNQRVAIKKISPFEHQTYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ORTLREIQILLRERHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 VP-GEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                 ELIFQETARFQPG 354
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ELIFEETARFQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular signal-regulated kinase (EC 2.7.-.-) 2 - common carp Nilternate names: CERK2
C.Species: Cyprinus carpio (common carp)
C.Species: Cyprinus carpio (common carp)
C.Apte: 13.-Un-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C.Accession: JW0053
R.Hashimoto, H.; Yokoyama, Y.; Matsuo, Y.; Toyohara, H.; Kohno, M.; Sakaguchi, M.
J. Blochem. 123, 1031-1035, 1998
A.Title: Existence of two isoforms of extracellular signal-regulated kinase in fish.
A.Fitler: Existence of two isoforms of extracellular signal-regulated kinase in fish.
A.Faccession: JW0053
A.Accession: JW0053
A.Accession: JW0053
A.Accession: JW0053
A.Accession: JW0055
A.Faccesion: JW0055
A.Faccesion: JW0055
A.Faccession: JW0055
A.Facc
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                                                                                                                                                                                        121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                     107 VQDLMETDLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLLNTTCDL 166
                                                                                                                                                                                                                                                                                         KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                             KICDFGLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                           227 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNAD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TVAEEPFTFAMELDDLPKERL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 PKALDLLDKMLTFNPHKRIEVEAALAHPYLEQYYDPSDEPVAEAPLKFEMELDDLPKETL 346
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     NRPI FPGKHYLDQLNHILGILGSPSQEDLNCI INMKARNYLQSLPSKTKVAWAKLFPKSD
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Rixu, J.R.; Hamer, J.B.
Genes Dev. 10, 2696-2706, 1996
A;Title: WAP Kinase and CAMP signaling regulate infection structure formation and pathoge
A;Reference number: Z25880; MUID:97102671; PMID:8946911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Acideule type: DAS AXUJ>
A;Reaidues: 1-356 <XUJ>
A;Cross-references: UNIPROT:Q92246; UNIPARC:UPI00006C824; EMBL:U70134; PIDN:AAC49521.2
A;Experimental source: strain Guyll
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                                                                                                                                       88 EIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFL 147
                                                                                                                                                                                                                                                                 208 RWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQE 267
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C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Pyricularia grisea
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51944
                                                                                                                                                                                                                                                                                                                                                           148 YOILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDVGPRYTQLQY1GEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 DLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathogenicity MAP kinase 1 [imported] - Pyricularia grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYLEQYYDPGDEPVCEEPFTLEMEFDDLPKEKLKELIWEE
72.4%; Pred. No. 2.5e-53; ive 38; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.6%; Score 932; DB 2; ilarity 53.4%; Pred. No. 5.8e-36; Conservative 55; Mismatches 79
                                  246; Conservative
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Best Local Similarity
Matches 181; Conserv
      Local Similarity
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          Best Loca
Matches
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A; Gene: sur-1
   A;Molecule type: mRNA
A;Residues: 1-376 <LMC>
A;Cross-references: UNIPROT:P39745; UNIPARC:UPI000002B465; GB:U27124; GB:S68B54; NID:g86
R;Jassal, B.; Smith, A.
submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                    A; Residues: 1-376 < WIL>
A; Residues: 1-376 < WIL>
A; Cross-references: UNIPARC; UP1000002B465; EMBL: Z46937; PIDN: CAA87057.1; GSPDB: GN00021;
A; Experimental source: clone F43C1
C; Genetics: A; Gene: mpk-1
A; Map position: 3
A; Map position: 3
A; Map position: 3
A; Naturons: 23/3; 43/2; 85/3; 104/2; 304/2
C; Superfamily: kinase-related transforming protein; protein kinase homology
C; Superfamily: phosphortansferase
C; Keywords: Afr; phosphortansferase
C; Keywords: Afr; phosphortansferase
C; S2D55 Domain: protein kinase homology < KIN>
F; 34-42/Region: protein kinase Afr-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP Kinase sur-1 (EC 2.7.1.-) - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Oc-Jan-1995 #sequence_revision O6-Jan-1995 #text_change O9-Jul-2004
CiAccession: A36977
R;Wu, Y.; Han, M.
R;Wu, Y.; Han, M.
R;Wu, Y.; Han, M.
A;Title: Suppression of activated Let-60 ras protein defines a role of Caenorhabditis A;Reference number: A36977; MUD:94131269; PMID:8299935
A;Retession: A36977; MUD:94131269; PMID:8299935
A;Retession: A36977; MUD:94131269; PMID:RD99835
A;Retession: A36977; MUD:PANDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTDARC:INTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DINCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRI----- 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 VEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQRTLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.1%; Score 1317; DB 2; Length 376; 72.4%; Pred. No. 2.2e-53; ive 38; Mismatches 36; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 PYLEQYYDPGDEPVCEEPFTLEMBFDDLPKEKLKELIWEE 353
                                                                                                                                                               A;Reference number: 219519
A;Accession: T22118
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 72.49
16; Conservative
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Matches 246;
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RESULT 14

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197

323

KARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVAE-

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70.1%; Score 1317; DB 2; Length 444;

Query Match

us-10-623-108-4.rpr

FTFAMELDDLPKERLKELIFQETAR 350	PEEFFDFDKHKDNLSKEQLKQFIYQEIMR 356
BP	PDDEPTAPP
324	318
ò	d

Search completed: February 6, 2006, 15:35:34 Job time : 27.8991 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                  Copyright
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OM protein - protein search, using sw model

February Run on:

6, 2006, 15:20:01; Search time 171.223 Seconds (without alignments) 1479.265 Million cell updates/sec

US-10-623-108-4 Perfect score:

1879 1 MAAAAAQGGGGEPRRTEGV......LKELIFQETARFQPGVLEAP 359 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1	mitogen-a	m mitogen-a	r mitogen-a	rattus norv	cricetulus	sapien	sapien	sapien	brachydanio	brachydanio	nus ca	bos taurus	homo sapien	gallus gall	mus musculu	rattus norv	pongo pygma	ous lae	ns lae	brachydanio	xenopus lae	nus ca	nus ca	orachydanio	orachydanio	brachydanio	tetraodon n	tetraodon n	aplysia cal	strongyloce	intes
tion	h mit	m mit	r mit	rattu	crice	homo	рошо	ношо	brach	brach	cyprinus	bos t	рошо	gallu	mus n	rattr	pongo	xenobna	xenobns	brack	xenog	cyprinus	cyprinus	brack	brack	brack	tetra	tetra	aplye	stror	ciona
Description	P27361	063844	P21708	04piy8	Q7m0h9	Q8nhx1	Q8nhx0	Q7z3h5	Q7zvk8	Q9dgr6	Q71zh4	P46196	P28482	O8nwg6	P63085	P63086	Q5nvr1	P26696	Q5d061	Q6p023	06d£k6	Q71zh5	061811	Q7zw72	Q9dgr5	Q4vh14	Q489m7	04 rv04	016945	Q8i892	Q4h315
1																															
	MK03 HUMAN	MK03 MOUSE	MK03_RAT	Q4PIY8 RAT	Q7M0H9 CRIGR	QBNHX1 HUMAN	28NHX0_HUMAN	Q7Z3H5 HUMAN	Q7ZVK8_BRARE	Q9DGR6_BRARE	Q7LZH4_CYPCA	01 BOVIN	MK01 HUMAN	QBUWG6_CHICK	MK01 MOUSE	MK01_RAT	QSNVR1_PONPY	MK01 XENLA	QSD061 XENLA	Q6P023_BRARE	Q6DFK6_XENLA	Q7LZH5_CYPCA	Q6I811_CYPCA	ZW72 BRARE	Q9DGR5_BRARE	24VH14_BRARE	4S9M7 TETNG	Q4RV04_TETNG	216945 APLCA	Q81S92_STRPU	Q4H3L5_CIOIN
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Length	379	380	380	380	369	357	332	323	392	391	392	360	360	368	358	358	358	361	361	369	361	369	369	369				366	351	369	350
* Query Match	98.9	95.1	94.9	94.9	94.0	9.68	84.8	83.1	82.6	•		81.9		81.8	81.3	ä	81.3	81.0	80.9	80.4	80.3	80.3	80.1	80.0	79.9	79.6	79.2	79.2	76.9	75.5	-
Score	1859	1787	1784	1784	1767	1683	1593	1561	1551.5	1550.5	1550.5					1528.5		-	-	-		1508	1506	1504	1501	1495	1488	1488	1445	1418	1399
Result No.	-	7	m	4	ស	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q8ayiO paralichthy Q86n95 marthasteri Q8mzz halocynthia P40417 drosophila Q7p159 drosophila Q5k4t9 meloidogyne Q60rp3 caenorhabdi P39745 caenorhabdi Q3558 mus musculu Q6pmm5 seristosoma Q7pvr1 anopheles Q87617 leptosphaer Q96x31 pyrenophora Q6r3q3 alternaria
QBAYIO PAROL QB6N95_MARGL QB6N95_MARGL QPKZ5_HALRO ERKA_DROME Q7PL59_DROME Q7PL59_DROME Q5K4T9_9BILA Q6K4T9_9BILA Q5K4T9_9BILA Q7PLS_CAEBR SUR1_CAEBL Q35558_MOUSE Q6PMMS_SCHJA Q7PRI_ANOGA Q87617_LEPMC Q96K313_9PLEO
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## ALIGNMENTS

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MEDILINE-2298257. PubMed=12477932; DOI=10.1073/pnas.242603899; MEDILINE-2298257. PubMed=12477932; DOI=10.1073/pnas.242603899; MEDILINE-2298257. PubMed=12477932; DOI=10.1073/pnas.242603899; MEDILINE-2298257. PubMed=12477932; DOI=10.1079/pnas.242603899; MEDILINE-2298257. PubMed=12477932; DOI=10.1079/pnas.242603899; MEDILINE-2298257. PubMed=1247927. Medine E., Mang J., Mang J., Haidh R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Raha S.S., Loquallano M.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.M., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Anilalon D.K., Muzny D.M., Sodergren B.D., Dickson M.C., Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anithing M., Madan A., Young A.C., Schwutz J., Myers R.M., C., Anithing M., Touchman J.W., Green B.D., Dickson M.C., A Schnetch A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Schmutz J., Myers R.M., Shenecch A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones B.D., Jones L.B., Jones S.J.M., Marra M.A., Schein J.B., Jones B.D., Jones L.B., Jones S.J.M., Marra M.A., Schein J.B., Jones B.D., Jones J.B., Jones J.B., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92171961; Pubmed-1540184;
Owaki H., Makar R., Boulton T.G., Cobb M.H., Geppert T.D.;
"Extracellular signal-regulated kinases in T cells: characterization
                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1993 (Rel. 25, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitogen-activated protein kinase 3 (EC 2.7.137) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase)
(MAP kinase 1) (MAPK 1) (P44-EKK1) (ERT2) (P44-MAPK) (Microtubule-associated protein 2 kinase).

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charest D.L., Jirik F., Harder K., Pelech S.L., Mordret G.; "Molecular cloning, expression, and characterization of the human mitogen-activated protein kinase p44erkl."; Mol. Cell. Biol. 13:4679-4690(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                        379 AA
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                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [3]
NUCLEOTIDE SEQUENCE OF 14-379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                  HUMAN
HUMAN
                                                       MK03
                                                  HERE REPRESENTED TO THE PROPERTY OF THE PROPER
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MK03 MOUSE
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STITITIES
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                                                                                                                               response to insulin and NGF. SUBUNIT: Binds to HIV-1 Nef. This interaction inhibits its kinase
                                          MEDLINE-92316223; PubMed-1319925; DOI=10.1016/0014-5793(92)80612-K; Gonzalez F.A., Raden D.L., Rigby M.R., Davis R.J.; "Heterogeneous expression of four MAP kinase isoforms in human
                                                                                                                                                                                                                                                                                                                           P53355:DAPK1; NDEXp=3; IntAct=EBI-73995, EBI-358616;
O75676:RPS6KA4; NDEXp=1; IntAct=EBI-73995, EBI-73933;
PTM: Autophosphorylated on threonine and tyrosine residues (By
                                                                                                                                                                                                                                                                                                                                                          similarity).
SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
kinase subfamily.
                                                                                                                                                                                                                                       (WAP27) (By similarity).
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
COPACTOR: Magnesium (By similarity).
ENZYME REGULATION: Activated and tyrosine phosphorylated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005524; F:ATP binding; NAS.
GO; GO:000524; F:ATP binding; NAS.
GO; GO:000468; P:Protein amino acid phosphorylation; IDA.
GO; GO:0000074; P:regulation of cell cycle; NAS.
InterPro; IPRO08349; Erk 1 2 MAPK.
InterPro; IPRO08351; JNK-MAPK.
InterPro; IPRO08357; MAP kin.
InterPro; IPRO08719; Prot kinase.
InterPro; IPRO08719; Ser thr pkin AS.
InterPro; IPRO08290; Ser thr pkin AS.
InterPro; IPRO08290; Ser thr pkinase.
           Commun. 182:1416-1422(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IntAct; P27361; -.
Ensembl; ENSG0000102882; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X60188; CAA42744.1; -; mRNA.
EMBL; BC013992; AAH13992.1; -; mRNA.
EMBL; M84490; AAA36142.1; -; mRNA.
PRSP; A40082; A46082.
HSSP; P204482; 1PME.
SMR; P27361; 29-374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1770; ERKIERKZMAPK.
PRINTS; PRO1772; JUKMAPKINASE.
PRODOM; PD000001; Prot_Kinase; 1.
SWART; SM00220; S_TKc; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS01017; PROTEIN_KINASE_ATP;
PROSITE; PS500117; PROTEIN_KINASE_DOM;
human ERK1 and ERK2 cDNAs.";
                                 NUCLEOTIDE SEQUENCE OF 25-379
                                                                                      FEBS Lett. 304:170-178(1992)
                                                                                                            INTERACTION WITH HIV-1 NEF.
of human ERK1 and ERK2
Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNC; HGNC:6877; MAPK3.
H-InvDB; HIX0012930; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reactome; P27361; -. MIM; 601795; -.
                                                                                                                                                                                                                                                                                                                INTERACTION:
                                                                                                                       PubMed=8794306;
                                                                                                                                                                                                                                                                                                       activity.
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                                                                              tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKALDLLDRMLTFNPNKRIT--------VABEPFTFAMELDDLPKERL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Cell cycle; Kinase; Nuclectide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.

DOMAIN

ACT SITE 166 166 Protein acceptor (By similarity).

ACT SITE 166 166 Proton acceptor (By similarity).

MOD_RES 202 202 Prosphothreonine (activates the kinase).

MOD_RES 204 204 Phosphothreonine (activates the kinase).

CONFLICT 174 174 17 1 -> S (in Ref. 1).

SEQUENCE 379 AA; 43136 MW; E6020CE413EC41F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL
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STRAIN=FVB/N; TISSUE=Kidney, and Mammary tumor;
STRAIN=FVB/N; TISSUE=Kidney, and Mammary tumor;
MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAAAAAQGGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels 20; Gaps
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25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitogen-activated protein kinase 3 (EC 2.7.1.37) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase)
(MAP kinase 1) (MAPK 1) (p44-ERK1) (ERT2) (p44-MAPK) (Microtubule-associated protein 2 kinase) (MNK1).

Musm=Mapk3; Synonyms=EFk1, Prkm3;
Musmusculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1859; DB 1; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                    380 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 KELIFQETARFQPGVLEAP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 359; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Q63844; 30-375

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M GOI GO: 0005737; C:Cytoplasm; IDA.

GO; GO: 0005737; C:Cytoplasm; IDA.

GO; GO: 0005634; C:nucleus; IDA.

GO; GO: 0005634; C:nucleus; IDA.

GO; GO: 0005634; C:nucleus; IDA.

GO; GO: 0001784; F:phosphotyrosine binding; IMP.

GO; GO: 0005515; F:protein binding; IPI.

GO; GO: 0005674; F:protein kinase activity; IDA.

GO; GO: 0005674; F:protein maino acid phosphorylation; IDA.

GO; GO: 0005674; P:response to DNA damage stimulus; IDA.

GO; GO: 0007165; P:signal transduction; TAS.

RO; GO: 0007165; P:signal transduction; TAS.

RICEPPO: IPR008349; Erk 1 2 MAPK.

RICEPPO: IPR008351; JMAP kin.

RICEPPO: IPR008351; JMAP kin.

RICEPPO: IPR000239; Ser_thr_pkin.AS.

RICEPPO: IPR000239; Ser_thr_pkin.AS.

RICEPPO: PR000239; Ser_thr_pkin.AS.

REALISTEAMPRINASE.

PRINTS; PR01772; JMKAPRINASE.

REALISTEAMPRINASE.

REALISTEAMPRINAS
                                                                                                                                    Ensembl; ENSMUSG0000063065; Mus musculus.
MGI; MGI:1346859; Mapk3.
EMBL; S58470; AAB19973.1; -; mRNA.
EMBL; X64605; CAA45889.1; -; mRNA.
                        EMBL; X64605; CAA4580
PIR; S28184; S28184.
HSSP; P28482; 1PME.
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BINDING
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NP BIND
ACT SITE
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                        Bosak S.A., McBwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S., Nones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CBA; TISSUB=Bone marrow; MBDIINE=9318591119(93)90411-U; MBDIINE=93185941; PubMed=8444355; DOI=10.1016/0378-1119(93)90411-U; BEBHIGH M.A., Nagorakaya T.V., Visser J.W.M., Belyavsky A.V.; Novel CDC2-related protein kinases produced in murine hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pubmed=8424957; DOI=10.1016/0167-4781(93)90074-N;
Tanner B., Mueckler M.;
"Molecular cloning of a mouse extracellular signal regulated kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pre-B cell;
MEDLINE=92020947; PubMed=1717989;
Crews C.M., Alessandrini A.A., Erikson R.L.;
"Mouse Erk-1 gene product is a serine/threonine protein kinase that has the potential to phosphorylate tyrosine.";
Proc. Natl. Acad. Sci. U.S.A. 88:8845-8849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91369479; PubMed=1716439; de Miguel C., Kligman D., Patel J., Detera-Wadleigh S.D.; de Miguel C., Kligman D., Patel J., Detera-Wadleigh S.D.; molyelecular analysis of microtubule-associated protein-2 kinase cDNA From mouse and rat brain...; DNA Cell Biol. 10:505-514(1991).
                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1171:319-320(1993)
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MEDLINE=93092802; PubMed=1459009;
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                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 4-380
                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stem cells.";
Gene 124:305-306(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fetal brain;
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Protein kinase.
ATP (By similarity).
ATP (By similarity).
ATP (By similarity).
Phosphothreonine (activates the kinase)

(By Bimilarity). Phosphotyrogine (activates the kinase) (By similarity).

205 203

72 205 178

5 and 6)

-> P (in Ref.

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                                                                                                                                                            122 ODLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLK 181
                                                                                                                                                                                                                                                                                                                     242 RPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDS 301
                                                                                                                                                                                                                                                                                                                                               243 RPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKCFPKSDS 302
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                                                                                                                                             HVRKTRVAIKKISPFEHOTYCORTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIV 121
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                                                                                                      2 AAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD
                                                                                                                                                                                                                                                              182 ICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSN
                                                       20; Gaps
                         95.1%; Score 1787; DB 1; Length 380; 91.8%; Pred. No. 1.8e-105;
                                                       Indels
380 AA; 43066 MW; 49C14A95B627237F CRC64;
                                        Pred. No. 1.8e-105;
1; Mismatches 10;
                                                          Matches 347; Conservative
                                             Local Similarity
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMHB outstation the European Bioinformatics. There are no restrictions on its use as long as its content is in no way modified and this statement is not

EMBL; BC013754; AAH13754.1; -; mRNA. EMBL; BC029712; AAH29712.1; -; mRNA.

removed.

PTM: Autophosphorylated on threonine and tyrosine residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase subfamily.

ENZYME REGULATION: Activated by tyrosine and threonine

phosphorylation.

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Belluscio L., la Monte S.M., Squinto S., Furth M.E., Yancopoulos G.D.,
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE OF 14-380, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=90312137; PubMed=2164259;
Boulton T.G., Yancopoulos G.D., Gregory J.S., Slaughter C., Moomaw C., Hsu J., Cobb M.H.;
                                                                                                                                                                                                                  MXO3 FAG:

MXO3 FAG:

MXO4 FAG:

MXO4 FAG:

01-MAY-1991 (Rel. 18, Created)

01-MAY-1991 (Rel. 25, Last sequence update)

13-SEP-2005 (Rel. 48, Last sequence update)

M14-Copen-activated protein kinase 3 (EC 2.7.1.37) (Extracellular signal-regulated kinase 1) (ERK-1) (Insulin-stimulated MAP2 kinase)

(MAP kinase 1) (MAP K) (p4-MAPK) (Microtubule-secciated protein 2 kinase) (MNKI).

Name-Mapk3; Synonyms=Erk1, Prkm3;

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUR=Brain;
MEDLINE=91013050; PubWed=1327976; DOI=10.1016/0378-1119(92)90109-3;
Marquardt B., Stabel S.;
"Sequence of a rat cDNA encoding the ERK1-MAP kinase.";
Gene 120:297-299(1992).
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Yung Y., Yao Z., Hanoch T., Seger R.;
"ERKIb, a 46-kDa ERK isoform that is differentially regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "An insulin-stimulated protein kinase similar to yeast kinases involved in cell cycle control."; Science 249:64-67(1990).
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PROTEIN SEQUENCE OF 43-64 AND 167-185, AND CHARACTERIZATION.
MEDLINE-91105092; Pubmed=1846291;
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MEDLINE=91369479; PubMed=1716439;
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NUCLEOTIDE SEQUENCE (ISOFORM B).
ELIFQETARFQPGVLEAP 359
                                                    363 ELIFQETARFOPGAPEGP 380
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Cricetulus.
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-i- FUNCTION: Kinase involved in a signal transduction pathway that activated by changes in the osmolarity of the extracellular environment. Plays an essential role in maintaining water homeostasis (By similarity).
-i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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R HSSP: A60041.

H HSSP: Q16539; 10-21.

R GO; G0:0005524; F:ATP binding; IEA.

GO; G0:0004685; F:Calcium- and calmodulin-dependent protein k. .;

R GO; G0:0004707; F:MAP kinase activity; IEA.

R GO; G0:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; G0:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; G0:0004674; F:protein amino acid phosphorylation; IEA.

InterPro; IPR008349; Erk 12 MAPK.

InterPro; IPR008351; JMK MAPK.

InterPro; IPR0003527; MAP kin.

InterPro; IPR00013527; MAP kin.

InterPro; IPR00013527; MAP kin.

InterPro; IPR008271; Ser_thr_pkin_AS.
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01-WAR-2004 (TrEWBLrel. 26, Last annotation update)
Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) ERK1
     Length 380;
                                                     Indels
y Match
94.9%; Score 1784; DB 2;
Local Similarity 91.8%; Pred. No. 2.7e-105;
hes 347; Conservative 1; Mismatches 10;
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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Q7M0H9;
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                                                       Protein kinase.

ATP (By similarity).

Proton acceptor (By similarity).

ATP (By similarity).

Phosphothreonine (activates the kinase)

(By similarity).

Phosphotyrosine (activates the kinase)

(By similarity).

E -> EVSRPPAAGRGISVPSVRPVPYCLCPQ (in
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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          Nucleotide-binding, Phosphorylation, Serine/threonine-protein kinase,
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EMBL; S46779; AAA11604.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1784; DB 1; Length 38 Pred. No. 2.7e-105; 1; Mismatches 10; Indels
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/FTId=VSP_004830.
G -> R (in Ref. 4).
53785C4ED722723A CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Extracellular-signal-regulated kinase 1.
Name-Mapk3;
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Q4PIY8;
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380 AA;
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Matches 347; Conserv
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Q8NHXO;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV033607; AAK52329.1; -; mRNA.
HSSP; P28462; IPME.
SMR; OBNHX1; 29-344.
SMR; OBNHX1; 29-344.
GO; GO:0005524; F:AFF binding; IEA.
GO; GO:0005524; F:AFF binding; IEA.
GO; GO:00046707; F:MAP kinase activity; IEA.
GO; GO:0006468; P:protein serine/threonine kinase activity; IEA.
InterPro; IPR008349; Erk_1_2_MAPK.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Extracellular signal related kinase 1b.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.0%; Score 1767; DB 2; Best Local Similarity 92.4%; Pred. No. 3.2e-104; Matches 341; Conservative 1; Mismatches 7;
PEINTS; PRO1069; Pkinase; 1.
PRINTS; PR01770; ERKIERKZMAPK.
PRINTS; PR01772; JNKMAPKINASE.
PRODOM; PD0000001; Prott kinase; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS01107; PROTEIN KINASE ATP; 1.
PROSITE; PS01010; PROTEIN KINASE ATP; 1.
PROSITE; PS01018; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-binding;
Serine, threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                      369
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY033608; AAK52330.1; -; mRNA.

REMBL; AY0331608; AAK52330.1; -; mRNA.

RHSSP; P20482; 1PWE.

R SMR; QBNIKO; 29-330.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:00045707; F:RAP kinase activity; IEA.

R GO; GO:00046707; F:RAP kinase activity; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004674; F:protein amino acid phosphorylation; IEA.

R InterPro; IPR008349; Erk_1 2_MAPK.

R InterPro; IPR0031527; MAP kin.

R InterPro; IPR00019; Prot_kinase.
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InterPro; IPR008351; JNK MAPK.
InterPro; IPR003527; MAP_kin.
InterPro; IPR000719; Prof. kinase.
InterPro; IPR000719; Prof. kinase.
InterPro; IPR0007290; Ser_thr_pkinase.
Prom; PR01770; BKNIBRKZMAPK.
PRINTS; PR01772; JNWANENINASE.
PROMO01; PR000001; Prof. kinase; 1.
SWART; SM00220; S TKC; 1.
PROSITE; PS01351; MAPK; UNKNOWN 1.
PROSITE; PS0010; PROTEIN KINASE APP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
A APT-binding; Kinase; Nuclectide-binding; Manage, Nuclectide-binding; Secure Application of Secure Application of Secure Application of Secure Application Applic
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Extracellular signal-related kinase 1c.
Homo sapiens (Human).
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PRINTS; PRO1770; ERKIERKZMAPK.
PRINTS; PRO1772; JNKMAPKINASE.
PRODOM; PD000001; Prot_kinase; 1.
SMART; SM01201; STK5; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS01011; PROTEIN KINASE DOM; 1.
PROSITE; PS01018; PROTEIN KINASE_ST; 1.
ATP-binding; Hypothetical protein; Kinase; Nucle Serine/threonine-protein kinase; Transferase.
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Q7ZVK8;
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                                                                                                                                                                                                                                                               VODIMETDLYKLLKSQOLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL 180
                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKALDLLDRMLTFNPNKRIT------VAEEPFTFAMELDDLPKERL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ALDLIDRMITFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERL 316
                                                                                                                                                                                                                                                 DHVRKTRVAIKKISPPEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                  VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                                                   KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                                                                                   NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted G.H. Amann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Kinase involved in a signal transduction pathway that is activated by changes in the osmolarity of the extracellular environment. Plays an essential role in maintaining water homeostasis (By similarity).

EMBL: SES37891; CAD97888.1; -; mRNA.
HSSP: Q16539; JO21.
SWR: Q723H5; 2-318.
Ensembl; ENSG0000102882; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                              1 MAAAAAQGGGGEPRRTEGYGPGVPGEVEMVKGQPFDVGPRYTQLQYIGBGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                 NRPIFPGKHYLDQLNHIL------
                                                                                                                                                                                                1 MAAAAAQGGGGGBPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                         Gaps
                                                                                                                                                                         64;
                                                                                                                                              84.8%; Score 1593; DB 2; Length 335;
82.8%; Pred. No. 3.1e-93;
ive 0; Mismatches 1; Indels 6.
                                                                                                                         38249 MW; A82027A684BA12E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-1004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp68600215 (Fragment).
            Pfam, PP00069; Pkinase; I.
PRINTS; PR01770; ERKIEKZMAPK.
ProDom; PD000001; Prot. Kinase; 1.
SMMRT; SM00220; S TKC; 1.
PROSITE; PS01351; MAPK; UNKNOWN 1.
PROSITE; PS00117; PROTEIN KINASE APP; 1.
PROSITE; PS00117; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 AA
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELIFQETARFQPGVLEAP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELIFOETARFOPGVLEAP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7Z3HS_HUMAN PRELIMINARY;
Q7Z3HS;
                                                                                                                                                              Best Local Similarity 82.8
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE=Human cervix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                          335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                          SEQUENCE
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                                                                                                                                                 Query Match
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DVYIVODEMETDLYKLLKSQOLSNDHICYPLYQILRGEKYIHSANVLHRDEKPSNLLINT 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKSDSKALDLLDRMLTFNPNKRIT-------VAEEPFTFAMELDDLP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSAYDHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Gaps
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Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Mitogen-activated protein kinase 3 (Extracellular signal-regulated
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004707; F:WAP kinase activity; IEA.

GO; GO:0004670; F:WAP kinase activity; IEA.

GO; GO:0006469; P:protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:ransferase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR008349; Erk 12 MAPK.

InterPro; IPR008357; MAP kin.

InterPro; IPR008271; MAP kin.

InterPro; IPR008271; Ser Ehr_pkin_AS.

InterPro; IPR002290; Ser Ehr_pkin_AS.

InterPro; IPR002290; Ser Ehr_pkin_AS.

InterPro; IPR002290; Ser Lhr_pkin_AS.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase, Nucleotide-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 83.1%; Score 1561; DB 2; Length 323; Local Similarity 93.8%; Pred. No. 3.2e-91; les 303; Conservative 0; Mismatches 0; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 AA; 37501 MW; 53D4EF00913948C1 CRC64;
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1;

307

367

173

67

53

233 247

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68 GWYCSAFDNYNKIRVAIKKISPFEHQTYCQRTLRBIKILLRFHHBNIIGINDILRARHID 127
                                                                                                                                                                                                                                              128 YMRDVYIVQDLMETDLYKLLKTQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLL 187
                                                                                                                                                                                                                                                                                                                                                                                                                           234 ILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ILAEMISNRPIFPGKHYLDQLNHILGVLGSPSQDDLNCIINMKARNYLQSLPQKPKIPWN
                                                                                                                                                                                                                                                                                                                     174 INTICOLKICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGC
                                                                                                                                                                                                                                                                                                                                                 9 AAAGAAGSNSSAAGPGGAVAPGGPSGAAGSKPG-LESVKGONPDVGPRYTDLQYIGEGAY
                                                                                                          GWVSSAYDHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLE
                                                                                                                                                                                                             114 AMRDVYIVQDLMBTDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 KLFPKSDSKALDLLDRMLTFNPNKRIT-------VAEEPFTFAMELD
  AAAAAQG------GGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirano T., Fujii R., Hibi M.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030902; BAB11812.1; -; mRNA.
HSSP; P28482; 1PME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLPKERLKELIFQETARFQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGDGR6_BRARE PRELIMINARY;
Q9DGR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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Altschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;
Schein J.E., Jones S.J.M., Marra M.A.;
Rodereation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. STRAIN-TUEDINGEN,

W. Krens S.F.G., Snaar-Jagalska B.E., Spaink H.P.;

"Cabrafish Erkl and ERK2.";

"Cabrafish Erkl and ERK2.";

"Cabrafish Erkl and ERK2.";

"Cabrafish Erkl and ERK2.";

"Mantred (FEB-2005) to the EMBL/GenBank/DDBJ databases.

R. BemBL; BC045505; AAH45505.1; -; mRNA.

R. BEMBL; BC06401; AAH66401.1; -; mRNA.

R. BEMBL; AY922319; AAY57804.1; -; mRNA.

R. SMR; PC28485; IPMR.

R. SMR; PC38485; IPMR.

R. SMR; PC38485; IPMR.

R. SMR; PC30004507; F:ATP binding; IEA.

GO; GO:0004707; F:ATP binding; IEA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:Protein amino acid phosphorylation; IEA.

R. GO; GO:0004674; F:Protein amino acid phosphorylation; IEA.

R. InterPro; IPR003527; MAP_Kin.

R. InterPro; IPR003527; MAP_Kin.

R. InterPro; IPR003290; Ser_thr_pkinase.

R. RiterPro; IPR004290; Ser_thr_pkinase.

R. Pram; PPR00669; Pkinase; I.

R. Pram; PPR00669; Pkinase; I.

PRIME PROME PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS001351; MAPK; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01770; ERKIERK2MAPK.
PRINTS; PR01772; JNKMAPKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Director MGC Project;
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NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Embryo;
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SEQUENCE
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Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                         R SNR; OBORR6; 40-385.

R ZFIN; ZDB-GENE-040121-1; mapk3.

R GO; GO:0004570; F:MAP binding; IEA.

GO; GO:0004670; F:MAP kinase activity; IEA.

GO; GO:0006669; P:protein serine/threonine kinase activity; IEA.

R GO; GO:0006669; P:protein serine/threonine kinase activity; IEA.

R GO; GO:0006669; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR008351; JMR MAPK.

R InterPro; IPR008351; JMAP kin.

R InterPro; IPR00819; Prot kinase.

R InterPro; IPR008219; Ser_thr_pkin_AS.

R InterPro; IPR008219; Ser_thr_pkin_AS.

R Pfam; PR0069; Prinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1770; ERRIBKEAMPE.
PRINTS; PRO1772; JNKMAPKINASE.
PRODOM; PRO1701; Proc. Kinase; 1.
SMART; SM00220; S.TRC; 1.
PROSITE; PS001351; MAPK; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
SEQUENCE 391 AA; 44126 MW; 6638F0807B5F9889 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%; Score 1550.5;
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Gaps

29;

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similarity).
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MK01 BOVIN
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                                                                                                                                                                                                                                         DLMETDLYKLLKTQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKI 195
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                                                                                                                                        VRKTRVAIKKISPPEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQ 122
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Sakaguchi M.;
"Existence of two isoforms of extracellular signal-regulated kinase in
                                                                                        SSAAGPGGAVAPGGPSGAAGSKPG-LESVKGQNPDVGPRYTDLQYIGEGAYGMVCSAFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALDLLDRMLTFNPNKRIT------VAREPFTFAMELDDLPKERLKE
                                                                                                                                                                                                                                                                                              CDFGLARIADPEHDHTGFLTEYVATRWYRAPBIMLNSKGYTKSIDIWSVGCILAEMLSNR
                                                               AAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQY1GEGAYGMVSSAYDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinus cárpio (Common carp).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Extracellular signal-regulated kinase (EC 2.7.-.-) 1 (Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB006038; BAD23842.1; -; mRNA.
Pred. No. 1.8e-90;
7. Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 AA
                           300; Conservative 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-FEB-2005 (TrEMBLrel. 29,
           81.18;
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Q7LZH4;
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LIFEETARFO 385
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HSSP; Q16539; 1021.
SMR; Q7LZH4; 39-386.
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           Best Local Similarity
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O71CZH4 CYP
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AC O71CZH
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51 GAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRAS 110
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C P46196; P46195; Rel. 32, Created)

TO 1-NOV-1995 (Rel. 32, Last sequence update)

TO 1-NOV-1995 (Rel. 32, Last sequence update)

TO 1-SPE-2005 (Rel. 48, Last annotation update)

TO 1-SPE-2005 (Rel. 48, Last annotation update)

Mitogen-activated protein kinase 1 (EEC 2.7.1.37) (Extracellular signal-regulated kinase 2) (MAPK 2) (p42-MAPK) (ERT1).

BE 3) (MAP kinase 2) (MAPK 2) (p42-MAPK) (ERT1).

Name-MAPK1; Synonyms-ERK2, PRKM1;

No Name-MAPK1; Synonyms-ERK2, PRKM1;

Bos taurus (Bovine)

C Mammalia; Eutheria; Laurasiatheria; Ctartiodactyla; Ruminantia;

C Pecora; Bovinae; Bos Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                        65 GAYGMVCSAFDNVNKIRVAIKKISPFEHQTYCQRTLREIKILLRFRHENIIGINDILRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 PWNKLFPKADNKALDLLDRMLTFNPIKRITVEBALAHPYLEQYYDPSDEPVAEBFTFNM
                                                                                                                                                                                                                                                                                                                                                            3 AAAAQGGGGGEPRRTEGVGPGV------PGEVEMVKGQPFDVGPRYTQLQYIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 NLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 NLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDMWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 VGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 VGCILAEMLSNRPIFFGKHYLDQLMHILGILGSPTQDDLNCIINMKARNYLQALPQKFKI
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-!- COFACTOR: Magnesium (By similarity).
-!- ENZYME REGULATION: Activated by phosphorylation on tyrosine and threonine in response to insulin and NGF.
-!- PTM: Autophosphorylated on threonine and tyrosine residues, which correlates with a slow and low level of autoactivation (By
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Phosphorylates microtubule-associated protein 2 (MAP2) Myelin basic protein (MBP), and Elk-1; may promote entry in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
TISSUB-AAFrenal medulla;
Ely C.M., Cox M.E., Her J., Parsons S.J.;
"Cloning and sequencing of ERK2 from a bovine adrenal medulla cDNA
                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                   2; Length 392;
                                                                                                                                                                                                                                                                                                 29; Indels
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Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Vuolencetide-binding; Kinase; Vuolencetide-binding; Serine/theonine-protein kinase; Transferase.
SEGUENCE 392 AA; 44133 MW; 02EE90132E5C347B CRC64;
                                                                                                                                                                                                                            Query Match

82.5%; Score 1550.5; DB
Best Local Similarity 78.5%; Pred. No. 1.8e-90;
Matches 300; Conservative 20; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 ELDDLPKEKLKELIYEETARFQ 386
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HUMAN
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                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
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                                                                                                                                                                                                                                              PRINTS; PR01770; ERKIERKZMAPK.
PRODOM; PD000001; Proct kinase; 1.
SMARY; SM00220; S.TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAAAAQGGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphothreonine (activates the kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
Phosphotyrosine (activates the kinase)
SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
E85D0B2A4E9549DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Protein kinase.
ATP (By similarity).
Poly-Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.9%; Score 1538.5; DB . 79.1%; Pred. No. 9.7e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Mismatches
                                                                                                                                                                           Interpro: IPR008349; Brk 1 2 MAPK.
Interpro: IPR008357; MAP Kin.
Interpro: IPR000719; Prof kinase.
Interpro: IPR008271; Ser thr pkin AS.
Interpro: IPR002290; Ser thr pkinase.
                                                                                                                       EMBL; Z14089; CAA78467.1; -; mRNA.
PPIR, S25011; S25011.
HSSP, P26482; 1PME.
SMR; P46196; 16-359.
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KELIFEETARFOPG 357
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Matches 296; Conservative
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               kinase subfamily.
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RESULT 13

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**XENUELDURS = 22288257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Chuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Chuler G.D., Alausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Rather D., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Dodden T.B., Toodhyuki S., Carninci P., Prange C., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raba S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J., Raha S.S., McKwam P.J., McKernan K.J., Mallek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Rhailing M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; Todeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
13-SEP-2005 (Rel. 24, Last sanctation update)
Mitogen-activated protein kinase 1 (EC 2.7.1.37) (Extracellular signal-requilated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP & 2) (MAP & Sinase 2) (MAP & 2) (MAP & Sinase 2) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92171961; PubMed=1540184; Cobb M.H., Geppert T.D.; Cwaki H., Makar R., Boulton T.G., Cobb M.H., Geppert T.D.; Extracellular signal-regulated kinases in T cells: characterization of human ERK1 and ERK2 COUMAs."; Biochem. Biophys. Res. Commun. 182:1416-1422(1992).
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"Human immunodeficiency virus type 1 Nef binds directly to LCK and
mitogen-activated protein kinase, inhibiting kinase activity.";
J. Virol. 70:6701-6708(1996).
-i. FUNCTION: Phosphorylates microtubule-associated protein 2 (MAP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myelin basic protein (MBP), and Elk-1; may promote entry in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=29216223; PubMed=1319925; DOI=10.1016/0014-5793(92)80612-K;
MEDLINE=29216223; Naden D.L., Rigby M.R., Davis R.J.;
"Heterogeneous expression of four MAP kinase isoforms in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
360 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 304:170-178(1992).
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STANDARD;
                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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KELIFQETARFQPG 354
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Best Local Similarity 79.1
Matches 296; Conservative
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         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWED outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                         R PRIMIS; PROUGOS; EXLINEAGE, 1.

R PRIMIS; PROUGOS; EXTRACE, 1.

R PROBOM; PROCOCOL; Proct_kinase; 1.

R ROSTITE; PROUGOS; TKC; 1.

R PROSITE; PSO1351; MAPK; 1.

R PROSITE; PSO1015; PROTEIN KINASE ATP; 1.

R PROSITE; PSO1001; PROTEIN KINASE DOM; 1.

R PROSITE; PSO1001; PROTEIN KINASE ST; 1.

R DOMAIN 25 313 PROTEIN KINASE.

T OWAPIN 25 313 PROTEIN KINASE.

T ACT SITE 149 149 PROTEIN KINASE.

T ACT SITE 149 149 PROTEIN KINASE.

T ACT SITE 149 PROTEIN KINASE.

T MOD_RES 185 185 Phosphothreonine (activates the kinase)

R MOD_RES 187 187 Phosphothreonine (activates the kinase)

T CONFLICT 91 91 R -> Q (in Ref. 2).
                                                                                        EMBL; M84489; AAA58459.1; -; mRNA.

EMBL; Z11694; CAA77752.1; -; mRNA.

EMBL; Z11695; CAA77753.1; ALT_INIT; mRNA.

EMBL; BCO17832, AAH17832.1; -; mRNA.

PIR; JQ1400; JQ1400.

PDB; IPME; X-ray; @=1-360.
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                                        removed
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QBUNGG;

QBUNGG;

QBUNGG;

QBUNGG;

QBUNGG;

QBUNGG;

QBUNGG;

QBUNGG;

QBUNGG;

QBUNGC;

QBUNGG;

QBUNGC;

CREMBLrel. 20, Last sequence update)

O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DATEAcellular signal-regulated kinase 2.

Extracellular signal-regulated kinase 2.

Extracellular (Chicken).

Extracellular (Chicken).

Extracellular (Chicken).

Extracellular (Chicken).

Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                     DHVRKTRVAIKKISPFEHQTYCORTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                               1 MAAAAAQGGGGGBPRRTEGVGPGVPGBVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                               37; Gaps
                                          81.9%; Score 1538.5; DB 1; Length 360; 79.1%; Pred. No. 9.7e-90; ive 18; Mismatches 23; Indels 37;
41390 MW; E85D0B2A5D2D724E CRC64;
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 SKALDLLDRMLTFNPNKRI-------T--TVAEEPFTFAMELDDLPKERL 340
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R RGSP; OBUNGG; 24-367.

R Ensembl; ENSGALGOOO01501; Gallus gallus.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004707; F:MAP kinase activity; IEA.

R GO; GO:0004644; P:protein serine/threonine kinase activity; IEA.

R GO; GO:0006464; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR008349; Erk 1 2 MAPK.

R InterPro; IPR00919; Prot kinase.

R InterPro; IPR00929; Ser_thr_pkinase.

R InterPro; IPR009290; Ser_thr_pkinase.
                                                                                                                           TISSUE-Pineal gland;
Kasahara T., Higashi C., Okano T., Fukada Y.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: ARS6503.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Indels 32;
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PRINTS; PRO1770; ERKIERKZMAPK.
PRODOM; PRO100001; Proc. kinase; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 KELIFOETARFOPG 354
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KELIFEETARFQPG 365
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Matches 295; Conservative
                                                                                                     NUCLEOTIDE SEQUENCE
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                                NCBI_TaxID=9031;
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MK01_MOUSE STANDARD; PRT, 358 AA P63085; P27703; Created) 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update)

RESULT 15
MK01_MOUSE
ID MK01_MC
AC P630B5
DT 01-AUGDT 01-AUG-

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Mitogen-activated process, Manages 1 (EC 2.7.1.37) (Extracellular Bignal-regulated Kinase 2) (MAPK 2) (BERK2) Mitogen-activated protein kinase 2) (MAPK 2) (BERK2) Mitogen-activated protein kinase 2) (MAPK 2) (BERK2) Mitogen-activated protein kinase 2) (MAPK 2) (PAPK) (BERT).

Samewalti Papulated Almas 2) (MAPK 2) (PAPK) (BERT).

Manamila Dantheria Dantchortoglires; Glires; Rodentia; Sciurcojnathi; Chammania Dantheria; Dantheria; Dantchortoglires; Glires; Rodentia; Sciurcojnathi; Chammania Dantheria; Dan
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Search completed: February
Job time : 172.223 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Involved in both the initiation and regulation of meiosis, mitosis, and postmitotic functions in differentiated cells by phosphorylating a number of transcription factors such as ELK-1. Phosphorylates EIF4EBP1; required for initiation of translation. Phosphorylates microtubule-associated protein 2 (MAP2) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

COPACTOR: Magnesium (By similarity).

COPACTOR: Magnesium (By similarity).

ENZYME REGULATION: Activated by phosphorylation on tyrosine and threonine in response to insulin and NGF. Both phosphorylations are required for activity (By similarity).

TISGUE SPECIFICITY: Widely expressed.

TISGUE SPECIFICITY: Widely expressed.

TISGUE SPECIFICITY: Midely expressed.

TISGUE SPECIFICITY: Midely expressed.

TISGUE SPECIFICITY: Midely expressed.
                                                                              STRAIN=CBA; TISSUE=Bone marrow;
MEDLINE=59158541; PubMed=8444355; DOI=10.1016/0378-1119(93)90411-U;
MEDLINE=591585941; PubMed=8444355; DOI=10.1016/0378-1119(93)90411-U;
Firbhler M.A., Nagorakaya T.V., Visser J.W.M., Belyavaky A.V.;
"Novel CDC2-related protein kinases produced in murine hematopoietic
                                                                                                                                                                                                                                                                           Payne D.M., Rossomando A.J., Martino P., Erickson A.K., Her J.-H. Shabanowitz J., Hunt D.F., Weber M.J., Sturgill T.W.; Identification of the regulatory phosphorylation sites in pp42/mitogen-activated protein kinase (MAP kinase)."; EMBO J. 10:885-892(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase subfamily.
                                                                                                                                                                                                                       PHOSPHORYLATION SITES THR-183 AND TYR-185, AND PARTIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0005534; C:Cytoplasm; IDA.
GO; GO: 0005534; C:nucleus; IDA.
GO; GO: 0005534; C:nucleus; IDA.
GO; GO: 0005534; C:nucleus; IDA.
GO; GO: 0005515; F:phosphotyrosine binding; IMP.
GO; GO: 0005515; F:phosphotyrosine binding; IMP.
GO; GO: 0005515; F:protein binding; IPI.
GO; GO: 00004672; F:protein kinase activity; IDA.
GO; GO: 00004672; F:protein kinase activity; IDA.
GO; GO: 00004672; F:protein amino acid phosphorylation; IDA.
GO; GO: 00006489; P:protein amino acid phosphorylation; IDA.
GO; GO: 00004689; P:signal transduction; TAS.
InterPro; IPR00329; P:signal transduction; TAS.
InterPro; IPR00329; PAP kin.
InterPro; IPR00319; Protein amino
InterPro; IPR00311; Ser thr pkin.
InterPro; IPR00311; Ser thr pkin.
InterPro; IPR00311; Ser thr pkin.
                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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PROSITE; PS01351; MAPK; 1.
PROSITE; PS01017; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
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EMBL; AK035386; BAC29053.1; -; mRNA.
EMBL; AK048127; BAC33251.1; -; mRNA.
EMBL; AK087925; BAC40044.1; -; mRNA.
EMBL; BC058258; AAH58258.1; -; mRNA.
EMBL; D10939; BAA01733.1; -; mRNA.
FR; S16444; S1444.
SNR; P65085; 14-357.
INTACt; P63085; -.
MGI; MGI:1346858; Mapkl.
                                                                                                                                                                                                                                                              MEDLINE=91184134; PubMed=1849075;
                                                            NUCLEOTIDE SEQUENCE OF 151-189.
    mouse cDNA sequences.";
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Gene 124:305-306(1993).
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PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Cell cycle; Direct protein sequencing; Kinase;
Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                   39; Gaps
                                                                                                                                                                                       the kinase)
                                                                      Protein kinase.

ATP (By similarity).

Poly-Alb similarity.

ATP (By similarity.

ATP (By similarity).

Phosphothreonine (activates the kinase).

Has phosphotyrosine (activates the kinase).

Has phosphotyrosine (activates the kinase).
                                                                                                                                                                                                                                                                         81.3%; Score 1528.5; DB 1; Length 358; 78.6%; Pred. No. 4.2e-89;
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KELIFEETARFOPG 355
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358 AA;
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COMPBIAS
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TELECOMMUNICATION INFORMATION:
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TELEFRAK: (202)408-4400
INPORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE:
US-08-622-277A-8
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                                                                  February 6, 2006, 15:34:56; Search time 36.2104 Seconds (without alignments) 819.670 Million cell updates/sec
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1 MAAAAAQGGGGEPRRTEGV.....LKELIFQETARFQPGVLEAP 359
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-411-628-14
US-10-174-794-14
US-09-625-580-25
US-09-642-749-25
US-09-417-197-39
US-09-417-197-39
US-08-417-197-57
US-08-417-197-57
US-08-415-953A-8
US-08-459-953A-8
US-08-459-953A-8
US-08-461-985-2
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US-08-458-887-2
US-08-932-012C-2
US-08-932-012C-2
US-08-933-12C-9
US-09-338-092-1028
US-09-538-092-1028
US-09-538-092-1028
US-08-461-862-4
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                  572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                       Run on:
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24 Sequence 4, App C-4 Sequence 4, App C-4 Sequence 4, App A-12 Sequence 12, App A-12 Sequence 12, App B-3 Sequence 12, App B-4 Sequence 34, App Sequence 35, App Sequence 35, App Sequence 35, App Sequence 35, App Sequence 35, App Sequence 36, App Sequence 36, App Sequence 36, App Sequence 36, App Sequence 16, App Sequence 16, App Sequence 16, App	-16 Sequence 16,	wh Kinase  *, Garrett &  on #1.30
US-08-458-887 US-08-932-787 US-08-822-217 US-08-622-217 US-08-457-040 US-08-457-040 US-09-457-040 US-09-417-197 US-09-417-197 US-09-427-040 US-09-427-040 US-09-427-040 US-09-427-040 US-09-427-040 US-09-642-749 US-09-642-749 US-09-642-749 US-09-642-749 US-09-642-749 US-08-61-985 US-08-61-985 US-08-91-085	US-08-932-012 ALIGNMENTS	cation US/08622277A  10N:  ni, Akiyoshi himori, Yuzo TION:  Rethod For Assaying MAP Kinas ENCES: 18 ADDRESS: Funcgan, Henderson, Farabow, Garret Pinnegan, Henderson, Farabow, Garret O I Street, N.W., Suite 700  ngton  A  STEM: Floppy disk EN PC compatible STEM: Floppy disk BN PC compatible STEM: Floppy disk ALOND MATA: ATA  27-MAR-1996 ON: 436 ON:
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                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10174794
; Sequence 14, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOWIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REPERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; PRIOR PELING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 379
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Pred. No. 1.2e-185;
0; Mismatches 0;
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Best Local Similarity 94.7%;
Matches 359; Conservative
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US-09-538-092-1021
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                                                                                                                                                                                                      VODLMETDLYKLLKSOOLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                   121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                                          KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                                                                                                                                                                                                                                                                                                                                                                                     NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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                                                                                                                       1 MAAAAAQGGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                     MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                              Gaps
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                      Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 1859; DB 2; Length 379; Best Local Similarity 94.7%; Pred. No. 1.2e-185; Matches 359; Conservative 0; Mismatches 0; Indels 2
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US-09-411-628-14

j Sequence 14, Application US/09411628

j Patent No. 6428994

j CENDREAL INFORMATION:
    CENDREAL INFORMATION:
    TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
    TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
    FILE REFERENCE: 13761-707

    CURRENT APPLICATION NUMBER: US 60/411,628

    CURRENT FILING DATE: 1999-10-01

    EARLIER APPLICATION NUMBER: US 60/102,906

    BARLIER PILING DATE: 1999-10-02

    NUMBER OF SEQ ID NOS: 16

    SOFTWARE: FastSEQ for Windows Version 4.0

    SEQ ID NO 14

    LENGTH: 379
                                                            Indels
                                                                ö
                    Query Match

98.9%; Score 1859; DB 2;
Best Local Similarity 94.7%; Pred. No. 1.2e-185;
Matches 359; Conservative 0; Mismatches 0;
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ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 596-9000
TELEPAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KELIFORTARFOPGVLEAP 379
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94.5%;
                                                                                                                                                                                                                                                                                                                                                                        379 amino acids
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Best Local Similarity 94.5
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                    CLASSIFICATION:
 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-025-580-25
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                                 COUNTRY:
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              GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION:
FILE REFREENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CLEAPALSEGFORMATHER Version 0.9
SEQ ID NO 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09025580

Sequence 25, Application US/09025580

Sexera No. 6162613

GENERAL INFORMATION:

APPLICANT: Wilson, Keith Phillip

APPLICANT: Wilson, Keith Phillip

APPLICANT: Wilson, Methods For Designing Inhibitors of

TITLE OF INVENTION: Methods For Designing Inhibitors of

TITLE OF INVENTION: Sexine/Thereonine Kinases and Tyrosine Kinase

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAAAAAQGGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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94.7%; Pred. No. 1.2e-185;
tive 0; Mismatches 0;
Sequence 1021, Application US/09538092
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Best Local Similarity 94.7
Matches 359; Conservative
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ORGANISM: Homo sapiens
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Pox, Ted
Wilson, Keith Phillip
Germann, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
Serine/Thereonine Kinases and Tyrosine Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
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ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1853; DB 2;
Pred. No. 5.2e-185;
0; Mismatches 1;
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Patent No. 6849716
GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-San
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US-09-417-197-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.6%; Score 1853; DB 2; Length 379; Best Local Similarity 94.5%; Pred. No. 5.2e-185; Matches 358; Conservative 0; Mismatches 1; Indels 2
                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                            ATTORNEY AGENTATION WUMBER: US/09/025,580
FILING DATE: cUnknown:
ATTORNEY AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                     STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/642,749
FILING DATE: 18-Aug-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
;
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-642-749-25
                                                                                       COUNTRY: US
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELIFOETARFOPGVLEAP 379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
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                                                    CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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RESULT 7 US-09-417-197-39 , Sequence 39, Application US/09417197

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Sequence 57, Application US/09417197

Batent No. 6518021

GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: On A Cellular Response
TITLE OF INVENTION: On A Cellular Response
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT PILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 57
                                                  To An Ir
GENERAL INFORMATION:

SENERAL INFORMATION:

A Method For Extracting Quantitative Information Relating TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 39
LENGTH: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...-----VAREPFTFAMELDDLPKERL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHVRKTRVAIKKISPPEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VQDLMETDLYKLIKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 VQDLMETDLYKGLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLSNTTCDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.6%; Score 1853; DB 2; Best Local Similarity 94.5%; Pred. No. 1.1e-184; Matches 358; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: mERK1-F64L-S65T-GFP fusion US-09-417-197-57
                                                                                                                                                                                                                                                                                                                                      FEATURE:
, OTHER INFORMATION: EGFP-Erkl fusion construct
US-09-417-197-39
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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241 OLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAMAKLFPKSDSKALDLLDRNLT 300
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                                                                                                                                                                                                                                                                                                                          133 LKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIAD 192
                                                                                                                                                                                                                                                                                                                                                                                                        193 PEHDHTGFLTRYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 QLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 FNPNKRIT------VAREPFTFAMELDDLPKERLKELIFQETARFQ 352
                                                                                                                                                                                               1 BPRGTAGVVPVVPGEVEVVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKK 60
                                                                                                                                                                                                                                                                 61 ISPFEHQTYCQRTLREIQILLGFRHENVIGIRDILRAPTLEAMRDVXIVQDLMETDLYKL
                                                                                                                                                            13 EPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKK
                                                                                                                      20;
                                                                           Length 367;
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Patent No. 5872006

GENERAL INFORMATION:
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Yancopoulos, George D.
APPLICANT: Aparayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/461,985 FILING DATE: 05-UN-1995 CLASSIFICATION: 800 PRIOR APPLICATION BDATA: PAPLICATION NUMBER: US 08/176,620 FILING DATE: 03-JAN-1994 ATTONNEY/AGENT INFORMATION:
                                                                           Score 1735; DB 1;
Pred. No. 1.1e-172;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 652
TELECOMMUNICATION INFORMATION:
                                                                                Query Match
Best Local Similarity 91.8%;
Matches 337; Conservative
TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGVLEAP 359
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                             ; MOLECULE TYP!
US-08-176-620A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-461-985-11
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                                                                                                                                                                                                                             QDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLK 181
                                                                                                                                                                                                                                                    123 QDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLK 182
                                                                                                                                                                                                                                                                                                             ICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSN 241
                                                                                                                                                                                                                                                                                                                                                                                           RPIFPGKHYLDQLWHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDS 301
                                                                                                                                                                                                                                                                                                                                                                                                                243 RPIFPGKHYLDQLAHILGILGSPSQEDLNCIINMKARNYLQSLFSKTKVAWAKLFPKSDS 302
                                                                                                                                             HVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIV 121
                                                                                      3 AAAAAPGGGGEPRGTAGVVPVVPGEVEVVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD 62
                                                                 AAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYD
                         20; Gaps
                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.8%; Pred. No. 8.8e-178;
tive 1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11, Application US/08176620A; Patent No. 5595904; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INPORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 6526-1
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELIFQETARFQPGVLEAP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELIFOETARFOPGAPEGP 380
                         Matches 347; Conservative
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-176-620A-11
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APPLICATION NUMBER: US/08/459,953A FILING DATE: June 2, 1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/029,494 FILING DATE: March 19, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lechner, Cornelia
Moller, Niels P.H.
Ullich, Axel
TITLE OF INVENTION: EXTRACELLULAR
                                                                                                                                                                                    209/267
                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 209/TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: (67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09393212
Patent No. 6579972
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE PORM:
                                                                                                                                                                                                                                                                                                                          LENGTH: 355 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4<sup>3</sup>
Matches 335, Conservative
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                            US-08-459-953A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-393-212-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ISPFEHQTYCQRTLREIQILLGFRHENVIGIRDILRAPTLEAMRDVIVQDLMETDLYKL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 LKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIAD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLNHILGILGSPSQEDINCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 QLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNPNKRIT-------VAEEPFTFAMBLDDLPKERLKELIFQETARFQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 EPRRIEGYGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKK 72
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                             Length 367;
                                                                                                                                                                                                                                                                                      9; Indels
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US-08-459-953A-8

Sequence 8, Application US/08459953A

Sequence 8, Application US/08459953A

Patent No. 6030822

GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: EXTRACELLULAR SIGNAL-RELATED
TITLE OF INVENTION: METHODS OF PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: G13 West Fifth Street
STREET: G14 Mest Fifth Street
STREET: California
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: SICORAGIE
                                                                                                                                                                                                                                             Score 1735; DB 1;
Pred. No. 1.1e-172;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.8*;
Matches 337; Conservative
                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-461-985-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 PGVLEAP 359
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61 TLREIQILLEFFHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEA 300
                                                                                                                                                                                                                                                          85 TLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHIC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRIT---- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 VATRWYRAPEIMINSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSP
                                                                                                                                                                      1 PGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR
                                                                                                                                                                                                                                                                                                                                                                                   145 YFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEY
                                                                                                                                                                                                                                                                                                                                                                                                                          121 YFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTFY
                                                                                                                                     25 PGEVENVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 ------VAEEPFTFAMELDDLPKERLKELIFQETARFQPGVLEAP 359
                                                                       20;
92.3%; Score 1734; DB 2; Length 355; 94.4%; Pred No. 1.3e-172;
                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINASE, SEQUENCES, AN
METHODS OF PRODUCTION
AND USE
                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
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204 180

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SOOLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 PFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VAEEPFTFAMELDDLPKERLKELIFQETARFQPG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 RRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Gaps
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Patent No. 5776731

GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
ITILE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                          COMPUTER KEALABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATYONENY/AGENT INPOMMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REBERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEPRAK: (212) 869-864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1723; DB 1;
Pred. No. 1.9e-171;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: (212) 869-8864/974
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.7%;
Best Local Similarity 91.8%;
Matches 335; Conservative 1
                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
: Pennie &
1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 PNKRIT----
          STREET: 1122
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 PGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 LAHPYLEQYYDPTDEPVAEEPPTFAMELDDLPKERLKELIFQETARFQPGVLEAP 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SECURICES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1734; DB 2;
Pred. No. 1.3e-172;
0; Mismatches 0;
                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,212
FILING DATE: 09-Sep-1999
CLASSIFICATION AUMER: 08/459,953A
APPLICATION NUMBER: 08/459,953A
FILING DATE: June 2, 1995
APPLICATION NUMBER: 08/029,494
FILING DATE: March 19, 1993
ATTORNEY AGENT INFORMATION:
REGISTRATION:
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08176620A; Patent No. 5595904; GENERAL INFORMATION: APPLICANT: Boulton, Teri G. APPLICANT: Yancopoulos, George D. APPLICANT: Nye, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8 :
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.4
Matches 335; Conservative
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US-08-176-620A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 PFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PFEHQTYCQRTLREIQILLGFRHENVIGIRDILRAPTLBAMRDVYIVQDLMETDLYKLLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNKRIT-----FQETARFQPG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGTAGVVPVVPGEVEVVKGQPFDVGPRXTQLQYIGEGAYGMVSSAXDHVRKTRVAIKKIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 RRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.7%; Score 1723; DB 1; Length 365; 91.8%; Pred. No. 1.9e-171; tive 1; Mismatches 9; Indels 2:
                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patent PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,862
FLING DATE: 05-UN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION 1973

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leelle
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELEPHONE: 212 790-9090
TELEPHONE: 212 869-8864/9741
TELEPHONE: 212 869-8864/9741
TELEPHONE: 66141 PENNIE
TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
TELECOMMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 91.8
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-463-862-2
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                                     New York
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Sequence 2, Application US/08461985 Patent No. 5872006 GENERAL INFORMATION: APPLICANT: Boulton, Teri G.

RESULT 15 US-08-461-985-2

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241 NHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFN 300
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APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Mye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie f 7
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COMPUTE: 10039
COMPUTE: Floppy disk
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COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/176,620
FILING DATE: 03-JAN-1994
ATTONEY/AGENT INPORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REJERRICE/POCKET NUMBER: 6526-123
TELECOMMULICATION INFORMATION:
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Best Local Similarity 91.8%; Pred. No. 1.9e-171;
Matches 335; Conservative 1; Mismatches 9;
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F: 1155 Avenue of the Americas
New York
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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TYPE: amino acid
TOPOLOGY: linear
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Search completed: February 6, 2006, 15:36:49 Job time : 37.2104 secs

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Sequence 19, App
Sequence 2, App
Sequence 2, App
Sequence 1421,
Sequence 1421,
Sequence 1456,
Sequence 1418,
Sequence 1418,
Sequence 1859,
Sequence 1819,
Sequence 1819,
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Sequence 1492,
                      Sequence
Sequence
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100.0%; Pred. No. 4.3e-147;
iive 0; Mismatches 0;
                                          US-10-072-036-41

US-10-64-421-19

US-10-64-421-19

US-10-64-421-19

US-10-76-149-4856

US-10-170-663-2

US-10-732-923-1421

US-10-732-923-1456

US-10-732-923-1436

US-10-732-923-1438

US-10-732-923-1367

US-10-732-923-1367

US-10-732-923-1367

US-10-732-923-1367

US-10-732-923-1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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ORGANISM: Homo sapiens
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US20040030110Alel Proteins and Nucleic Acids Encoding
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301 SKALDILIDRMILTENPNIKRITVAEEPFTFAMELDDLPKERLKELIFQETARFQPGVLEAP 359
                                                                                              ## APPLICANT: Stone, David J.
## APPLICANT: Stone, David J.
## APPLICANT: Stone, David J.
## APPLICANT: Stochenberg, Mark E.
## APPLICANT: Rothenberg, Mark E.
## APPLICANT: Rothenberg, Mark E.
## TILE OF INVENTION: NO. US20040030110Alel Proteins and Nucleic Acids Encorners Trills OF INVENTION: DATE: 2002-11-27
CURRENT FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 200
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99.7%; Pred. No. 1.4e-146;
cive 0; Mismatches 1;
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Publication No. US20030109419A1
GENERAL INFORMATION:
                             Rastelli, Luca
Edinger, Shlomit R.
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Best Local Similarity 99.7
Matches 358; Conservative
                                                                                  Stone, David J
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US-10-114-270-110
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US-10-233-448-7
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                                                                                           GENE VARIANTS ASSOCIATED WITH CANCERS
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DAI, KEN-SHWO
TITLE OF INVENTION: HUMAN SMAPK3-RELATED GE
CURRENT APPLICATION NUMBER: US/10/623,108
CURRENT APPLICATION NUMBER: 2003-07-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 110, Application US/10114270; Publication No. US20040030110A1; GENERAL INFORMATION:
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
Padigaru, Muralidhara
Shimkeers, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Csman, Stacie J.
Ji, Weizhen
Anderson, David W.
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APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.'
Matches 359; Conservative
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Vernet, Corine
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CORGANISM: Homo sapiens
US-10-623-108-8
                                                                                                                                                                                                                                                                                            CENGTH: 359
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359; Conservative
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                                                                                                                                                                                                                                                                         Gaps
APPLICANT: Fisone, Gilberto
TITLE OF INVENTION: METHOD FOR CLASSIFICATION OF ANTI-PSYCHOTIC DRUGS
FILE REPERENCE: 11181-009
CURRENT APPLICATION NUMBER: US/10/233,448
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 60/316,338
PRIOR APPLICATION NUMBER: 60/316,338
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
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i Sequence 14, Application US/10174794

j Publication No. US20030166220A1

i GENERAL INFORMATION:

APPLICANT: University of Southern California

i TITLE OF INVENTION: EBGUENCES OF LEARNING-INDUCED RIVASES

FILE REFERENCE: 13761-707

i CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US/09/411,628

PRIOR APPLICATION NUMBER: US 60/102,906

PRIOR PILING DATE: 1999-10-01

PRIOR PILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

i SOFTHARE: FastSEQ for Windows Version 4.0

i EBNGTH: 379
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                                                                                                                                                                                                                                          Length 379;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                     Query Match

98.9%; Score 1859; DB 4;
Best Local Similarity 94.7%; Pred. No. 2.1e-145;
Matches 359; Conservative 0; Mismatches 0;
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                                                                                                                                                                                          ORGANISM: Homo sapiens
US-10-233-448-7
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Best Local Similarity
                                                                                                                                                             LENGTH: 379
TYPE: PRT
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Sequence 10, Application US/10394322A
Sequence 10, No. US20030232391A1
GENERAL INPORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFREENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US 60/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
TYPE: PRI
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  0; Mismatches
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Best Local Similarity 94.7
Matches 359; Conservative
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GENERAL INFORMATION:
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241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINWKARNYLQSLPSKTKVAWAKLFPKKD 300
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GLIOBLASTOMA PROGRESSION
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94.7%; Pred. No. 2.1e-145;
iive 0; Mismatches 0;
                                                                                                                                                                                                                          Sequence 8, Application US/10701490

Sequence 8, Application US/10701490

Sequence 8, Application No. US20040106141A1

GENERAL INFORMATION:

APPLICANT: FAUL S. MISCHEL

APPLICANT: CHARLES L. SAWYERS

APPLICANT: KATHERINE CROSBY

TITLE OF INVENTION: METHODS AND MATERIALS FOR EXA

TITLE OF INVENTION WHERE: 2003-11-05

PRIOR APPLICATION NUMBER: 60/423,777

PRIOR FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 8

SEQ ID NO 8
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US-10-35-118-3
; Sequence 3, Application US/10735118
; Publication No. US20040248151A1
                                                                                                                                      361 KELIFQETARFQPGVLEAP 379
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Best Local Similarity
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APPLICANT: Bacus, Sarah S.
APPLICANT: Bacus, Sarah S.
APPLICANT: Bacus, Sarah S.
APPLICANT: Smith, Bradley L.
TITLE OF INVENTION: METHOD FOR PREDICTING THE RESPONSE TO HER2-DIRECTED THERAPY FILE OF INVENTION: METHOD FOR PROJECTION NUMBER: US/10/735,118
CURRENT APPLICATION NUMBER: US/370,473
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 3
SOPTWARE: Patentin Version 3.1
SEQ ID NOS: 3
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Sequence 6, Application US/10623108

Publication No. US20050013817A1

GENERAL INFORMATION:

APPLICANT: DAI, KEN-SHWO

TITLE OF INVENTION: HUMAN SMAPK3-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS

FILE REFERENCE: U 014726-8

CURRENT APPLICATION NUMBER: US/10/623,108

CURRENT FILING DATE: 2003-07-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 379
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Matches 359; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-623-108-6
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y APPLICANT: Al waramacusus
APPLICANT: Relichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-Tchi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Oun-Ichi Nezu
TITIE OP INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/10/060,065
CURRENT APPLICATION NUMBER: US 60/189,590
PRIOR PLILING DATE: 2000-07-28
PRIOR PLILING DATE: 2000-07-28
PRIOR PLILING DATE: 1999-10-18
PRIOR PLILING DATE: 2000-02-17
PRIOR PLILING DATE: 2000-02-17
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 16
SEQ ID NO 16
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            --VAEEPFTFAMELDDLPKERL 340
                              1 MAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
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                                                                                                                                                      RESULT 11
US-10-060-065-16
i Sequence 16, Application US/10060065
i Publication No. US20030017480A1
i GENERAL INFORMATION:
i APPLICANT: Toshio Ota
i APPLICANT: Tetuo Nishikawa
non:TCANT: Tetuo Nishikawa
                                                                             341 KELIFOETARFOPGVLEAP 359
                                                                                                             361 KELIFQETARFOPGVLEAP 379
              SKALDLLDRMLTFNPNKRIT
                                                                                                                                                                                                                                                                                                                                       Jun-Ichi Yamamoto
Shizuko Ishii
                                                                                                                                                                                                                                                                                                                                                                         Tomoyasu Sugiyama
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Best Local Similarity 94.5
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                     Kaoru Otsuka
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TYPE: PRT
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                                                 1 MAAAAAQGGGGGEPRRIEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                   1 MAAAAAQGGGGEPRRTEGVGPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAY
                 Gaps
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Publication No. US20050095657A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Methods and Kits for Detecting Proteins
FILE REFERENCE: 50508-2280
CURRENT APPLICATION NUMBER: US/10/945,684
CURRENT FILING DATE: 2004-09-21
CURRENT PILING DATE: 2004-09-21
SOFTWARE: Patentin version 3.2
SEQ ID NO 2.
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               Indels
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 Pred. No. 2.1e-145;
0; Mismatches 0;
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94.78;
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 Best Local Similarity 94.7
Matches 359; Conservative
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ORGANISM: Homo Sapiens
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TITLE OF INVENTION: Methods For Designing Inhibitors of
                                                  KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                             KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                            241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/170,663
FILING DATE: 12-Jun-2002
CLASSIFTCATION DATA:
APPLICATION NUMBER: 09/025
FILING DATE: CUNKNOWN>
PRIOR APPLICATION NUMBER: 09/025,580
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97-104
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
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US-10-170-663-25
; Sequence 25, Application US/10170663
; Publication No. US2030165899A1
; GENERAL INFORWATION:
; APPLICANT: Su, Michael Shin-San
; Prof. Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 596-9000
TELEFAX: (212) 596-9090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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       181 KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS 240
                                                     NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
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TITLE OF INVENTION: MOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILER REFERENCE: 0650.109800.
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-11
PRIOR APPLICATION NUMBER: US 60/18776
PRIOR PLING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 600-183767
PRIOR FILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR PLILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
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Pred. No. 6.6e-145;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 379
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/10059585 Publication No. US20030082776A1 GENERAL INFORMATION:
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Funahashi, Shin-Ichi
Senoo, Chiaki
Nezu, Jun-Ichi
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Nishikawa, Tetsuo
Hayashi, Koji
Otsuka, Kaoru
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Best Local Similarity 94.5%;
Matches 358; Conservative
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Ishii, Shizuko
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Nagai, Keiichi
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US-10-059-585-37
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Best Local Similarity
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US-10-059-585-37
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APPLICANT:
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RESULT 15
US-10-072-036-39
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                                        KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
                                                                                                                                                                                                           Germann, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of Serine/Thereonine Kinases and Tyrosine Kinase
                           DHVRKTRVAIKKISPFEHOTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI
                                                                                                                                       KICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPTRY: US

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/893,072

FILING DATE: 15-Jul-2004

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: VPI 97-104
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APPLICATION NUMBER: US/09/642,749
FILING DATE: 18-Aug-2000
APPLICATION NUMBER: US/09/025,580
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, Keith Phillip
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/10893072
Publication No. US20040259166A1
GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of t
                                                                                                                                                                                                                                                                                                                           LENGTH: 379 amino acids
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SEQUENCE CHARACTERISTICS:
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US-10-893-072-25
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TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An ITITLE OF INVENTION: On A Cellular Response
TITLE OF INVENTION: On A Cellular Response
FILE REPERBENCE: 3759-0120P
CURRENT APPLICATION NUMBER: US/10/072,036
CURRENT FILING DATE: 2002-09-13
PRIOR PELLING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SSGTWARE: Patentin version 3.0
SSGTWARE: Patentin version 3.0
SEQ ID NO 39
LENGTH: 631
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                                                                                                             Length 379;
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                                                                                                          Score 1853; DB 5;
Pred. No. 6.6e-145;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: EGFP-Erk1 fusion construct
, MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-893-072-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 SKALDLLDRMLTFNPNKRIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/10072036 Publication No. US20030082564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 KELIFQETARFQPGVLEAP 359
                                                                                                             Query Match 98.6%;
Best Local Similarity 94.5%;
Matches 358; Conservative
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Best Local Similarity 94.5
Matches 358; Conservative
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APPLICANT: Soren TULLIN
APPLICANT: Kasper ALMHOLT
APPLICANT: Kurt SCUDDER
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Search completed: February 6, 2006, 15:40:57 Job time : 126.184 secs

Sequence Sequence Sequence Sequence Sequence

Sequence 261, App Sequence 8, Appli Sequence 9, Appli Sequence 10, Appli Sequence 268, App Sequence 27, App Sequence 391, App Sequence 391, App Sequence 392, App Sequence 271, App Sequence 271, App Sequence 25, App Sequence 26, App

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APPLICANT: Al marameteral
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Chiaki Senoo
PELICANT: Chiaki Senoo
APPLICANT: Chiaki Senoo
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: NOVEL GENES: US/11/109,156
CURRENT PELICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-03
PRIO
                                                                                  US-10-770-726-65
US-11-024-959-267
US-11-024-959-267
US-11-024-959-261
US-10-786-065-9
US-10-786-065-9
US-11-024-959-268
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US-11-024-959-268
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Publication No. US20050250144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUblication No. US20050250144A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Tetao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
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Shizuko Ishii
Tomoyasu Sugiyama
Ai Wakamatsu
Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
Chiaki Senoo
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      February 6, 2006, 15:37:06 ; Search time 10.8631 Seconds
(without alignments)
387.254 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                            1 MAAAAQGGGGEPRRTEGV......LKELIFQETARFQPGVLEAP 359
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1: /cgn2 6/ptodata/1/pubpaa/USO8 NEW FUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/USO6 NEW FUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO7 NEW FUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/DSO7 NEW FUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USO9 NEW FUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USO1 NEW FUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USO1 NEW FUB.pep:*

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8: /cgn2 6/ptodata/1/pubpaa/USO1 NEW FUB.pep:*
                                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-878-556A-134
US-11-186-26A-115
US-10-878-329-1
US-10-87-70-726-69
US-11-127-817-18
US-11-127-817-18
US-11-127-817-19
US-11-127-817-19
US-11-024-959-265
US-11-024-959-272
US-11-034-959-272
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US-11-024-959-393
US-11-024-959-395
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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APPLICANT: Berger, Allison
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APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Sanitar, Subhangi
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: MERRAPY OF COLON CANCER
TITLE OF INVENTION: MERRAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: MERRER: US/10/301,822
FRIOR FILING DATE: 2002-01-21
FRIOR FILING DATE: 2001-11-10
FRIOR APPLICATION NUMBER: US 60/381,988
FRIOR FILING DATE: 2002-03-05
FRIOR FILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 DNVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRHENIIGINDIIRAPTIEQMKDVXI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSKNLLINTTCDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRPRHENVIGIRDILRASTLEAMRDVYI 120
                                                           224 NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNAD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKALDLIDRMLTFNPNKRITV-------AEEPFTFAMELDDLPKERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.9%; Score 1538.5; DB 7; Length
79.1%; Pred. No. 3.3e-129;
.ive 18; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 115, Application US/11186284
; Publication No. US20050266493A1
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                          341 KELIFQETARFQPG 354
                                                                                                                                                                                                                                                                                                         |||||:|||||||
344 KELIFEETARFQPG 357
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Best Local Similarity 79.11
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo Sapiens
US-11-186-284-115
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                                                                                                                                                                                                                                              61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                61 DHVRKTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILRASTLEAMRDVYI 120
                                                                                                                                                                                                                                                                                                                                                                     VQDLMETDLYKLIKSQQLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLINTTCDL 180
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                                                                                                                                                            1 MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAX
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                                                                                                                       1 MAAAAAQGGGGGPRRTEGVGPGVPGVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAY
                                                                 Gaps
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Length 379;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 134, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; TITLE REFERENCE: 21762
; CURRENT FILING NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 134
; LENGTH: 360
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
Score 1853; DB 7;
Pred. No. 4.4e-157;
0; Mismatches 1;
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81.9%; Score 1538.5; DB 6
Best Local Similarity 79.1%; Pred. No. 3.3e-129;
Matches 296; Conservative 18; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw_hum/mk01_human
DATABASE ENTRY DATE: 1992-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 KELIFQETARFQPGVLEAP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 KELIFQETARFQPGVLEAP 379
   Query Match 98.6%;
Best Local Similarity 94.5%;
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-878-556A-134
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APPLICANT: KAWARER, STEFAN M.
APPLICANT: KAWARER, STEFAN M.
APPLICANT: KAWARER, STEFAN M.
APPLICANT: RELSON, MATTHEW ROBERTS
APPLICANT: RENELAND: RIXARD HERRY
TYPLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: WETHOOS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: WETHOOS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: WETHOOS FOR 100723,681
FRICK APPLICATION NUMBER: US/10/23,681
FRICK FILING DATE: 2003-07-24
FRICK FILING DATE: 2003-07-24
FRICK FILING DATE: 2003-11-25
FRICK APPLICATION NUMBER: 60/490,234
FRICK FILING DATE: 2003-11-25
SEQ ID NOS: 4962
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 21
LENGTH: 422
                                                                                                                                                                                                                                                                                                                            42 YTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLRFRHENV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 ANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 KGYTKSIDIWSVGCILAEMLSNRPIFPCKHYLDQLNHILGILGSPSQEDLNCIINMKARN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|||| : :||||: :||||258 YIQSLPRKDFTQLFPRAPEBE 317
                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 MHYNQTVDIWSVGCIMAEMLTGKTLFKGKDYLDQLTQILKVTGVPGTEFVQKLNDKAAKS
                                                                                                                                                                                                                                                                                                                                                         25 YVSPTHVGSGAYGSVCSAIDKRSGEKVAIKKLSRPFQSEIFAKRAYRELLLLKHMQHENV
                                                                                                                                                                                                                                                                                                                                                                                                                           101 IGIRDILR-ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILRGLKYIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 YLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.5%; Score 629; DB 6; Length 422; 39.7%; Pred. No. 2e-48; ive 72; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                              Query Match 37.5%; Score 704.5; DB 6; Best Local Similarity 42.8%; Pred. No. 3.3e-55; Matches 143; Conservative 64; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 --AEEPFTFAMELDDLPKERLKELIFQETARFQP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 69
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: ROTH, RICHARD B. APPLICANT: BRAUN, ANDREAS
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Best Local Similarity 39.7%
Matches 138; Conservative
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                                                                                                                                                                                          US-10-770-726-69
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
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                               FRHENVIGIRDILR-ASTLEAMRDVYIVQDLMBTDLYKLLKSQQLSNDHICYFLYQILRG 153
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                                                                                                                                                                                                                                                                 Sequence 1, Application US/10886329; Publication No. US20050288286A1; GENERAL INFORMATION:
            SKALDLLDRMLTFNPNKRITV-
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344 KELIFEETARFOPG 357
                                                                                                    KELIFOETARFOPG 354
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US-10-770-726-69
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APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Lacmen, Mendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: 80/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR PAPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
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US-11-127-817-19

Sequence 19, Application US/11127817

Publication No. US20050287519A1

GENERAL INFORMATION:

APPLICANT: Mcrinice Peacal G.

APPLICANT: Hoffmann, Marcel

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Taleann, Wendy

TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting

TITLE OF INVENTION: Amyloid-Beta Protein Production
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                                                                               350 VDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKE
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39.7%; Pred. No. 2e-48;
tive 72; Mismatches 94; Indels
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                                                                                                                                                                                     ; Sequence 20, Application US/11127817; Publication No. US20050287519A1; GENERAL INFORMATION:
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Best Local Similarity 39.7
Matches 138; Conservative
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CRGANISM: Homo sapiens
US-11-127-817-20
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US-11-127-817-20
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APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REPERENCE: P27, 800-D USA
CURRENT APPLICATION NUMBER: 60/570,352
PRIOR PILING DATE: 2004-05-12
PRIOR PILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/639,948
PRIOR PILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: PATCH IN VERSION 3.3
SEQ ID NO 18
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                          36 FDVGPRYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLR
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APPLICANT: GRIGOR, WIRRAY ROBERT
APPLICANT: GRIGOR, WIRRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: LUND, STEVEN TROY
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: CONNETT, ANDREAS
APPLICANT: CONNETT, ANDREAS
APPLICANT: CONNETT, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REPRENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
                                                                                                                                                                                                                                                                           94; Indels
                                                                                                                                                                                                                                          33.5%; Score 629; DB 7;
39.7%; Pred. No. 2.3e-48;
tive 72; Mismatches 94;
           CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR PILING DATE: 2004-05-12
PRIOR PILING DATE: 2004-05-12
PRIOR PILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: PatentIn version 3.3
LENGTH: 464
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PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FORSTER, RICHARD L.
 FILE REFERENCE: P27,800-D USA
                                                                                                                                                                                                                                                          Best Local Similarity 39.7
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-817-19
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LENGTH: 460
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                                                                                                                                                                                                                                               Query Match
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26.1%; Score 491; DB 7; Length 460; 38.3%; Pred. No. 3.9e-36;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 IHSANVIHRDLKPSNILIN-TTCDLKICDFGLARIADPEHDHTGF-----LTEYVATRW 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 CHSHRVLHRDLKPONLLLDRRTNSLKLADFGLAR-----AFGIPVRTFTHEVVTLW 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 YRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGRHYLDQLAHILGILGSPSQEDL 269
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                                                                                                                                                                        213 PEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 QYEKIEKIGEGTYGVVYKAIDRSTNKTIALKKIRLEQEDEGVPSTAIREISLIKEMQHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 RYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLRFRHEN
                                                41 RYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKISPFEHQTYCQR---TLREIQILLRFRH
                                                                            156 YIHSANVIHRDLKPSNLLINTTCDL-KICDFGLAR--IADPEHDHTGFLTEYVATRWYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                        273 INMKA-RNYL--OSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVAE---EPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 263 Application US/11024959
; Beducence 263 Application US/11024959
; Publication No. US2006010516A1
; GENERAL INFORMATION:
    APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: GRIGOR, MRRAY ROBERT
; APPLICANT: HIGGINS, COLLERN M.
; APPLICANT: HIGGINS, COLLERN M.
; APPLICANT: HIGGINS, COLLERN M.
; APPLICANT: HOSTISM, ANDREAS
; APPLICANT: WORZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED
; CURRENT FILING DATE: 2004-12-30
; PRIOR PLING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PARENTIN VORSING: 3:3
; SEQ ID NOS: 782
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91,
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Best Local Similarity 38.6%; Pred. No. 2.4e-36;
Matches 115; Conservative 50; Mismatches 92
  Mismatches
  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Eucalyptus sp. US-11-024-959-263
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version 3.3
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292 -FKDIP-DNLKKL 302
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Matches 117; Conservative
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Best Local Similarity 37.77
Matches 109; Conservative
                                                                             ; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-264
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ORGANISM: Eucalyptus sp.
NUMBER OF SEQ ID NOS
SOFTWARE: PatentIn v
SEQ ID NO 264
LENGTH: 304
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 IHSANVLHRDLKPSNLLIN-TTCDLKICDFGLARIADPEHDHTGF-----LTEYVATRW 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 YRAPEIMINSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 YRAPEILLGSRHYSTPVDVWSVGCIFAEMVNQRPLFPGDSEIDELFKIFRILGTPNEDTW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 RYTQLQYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCQRTLREIQILLRFRHEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 PGVTALP--DFKSAFPKWPAKNLQDMVPGLNSAGIDLLSKMLCLDPSKRIT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 481.5; DB 7; Length 294; Best Local Similarity 37.8%; Pred. No. 1.5e-35; Matches 110; Conservative 55; Mismatches 99; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Squence 264, Application US/11024959

Squence 264, Application US/11024959

Publication No. US20060010516A1

GENERAL INFORMATION:

APPLICANT: PORSTER, RICHARD L.

APPLICANT: EMERSON, SARAH JANE

APPLICANT: GRIGGINS, COLLEEN M.

APPLICANT: HIGGINS, COLLEEN M.

APPLICANT: HOGGINS, COLLEEN M.

APPLICANT: KODRXYCKI, BOB

TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS:

TITLE OF LING JA463-0360

CURRENT APPLICATION NUMBER: US/11/024,959

CURRENT FILING DATE: 2004-12-30

PRIOR PLING DATE: 2003-12-30
                                                                                                                                  APPLICANT: FORCETS, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGOR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: LUND, STEVEN TROY
APPLICANT: MAGUSIN, ANDRES
APPLICANT: KODISTN, ANDRES
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILLE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILLING DATE: 2004-12-30
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PATENTIN VERSION 3.3
                                                                           Sequence 265, Application US/11024959
Publication No. US20060010516A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Eucalyptus sp.
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US-11-024-959-264
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LENGTH: 294
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100 VIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKS---QQLSNDHICYFLYQILRGLKY 156
                                                                                                                                                                                                      100 VIGIRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDH--ICYFLYQILRGLKYI 157
                                                                                                                                                                                                                                     158 HSANVIHRDLKPSNILINTTCDLKICDFGLAR-IADPEHDHTGFLTEYVATRWYRAPEIM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 --KARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRI---TVAEEPFTFAM 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 DWKPENF-EKYPGE---PLNKVCPKMDPDGLDLLDKMLKCNPSERIAAKNAMSHPY---- 291
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                                                                                                 41 RYTOLOYIGEGAYGMVSSAYDHVRKTRVAIKKIS-PFEHQTYCORTLREIQILLRFRHEN 99
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                                                                                                                                                                                                                                                                                                                                                                                                            217 INSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINM-
  Length 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGON, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: HOGGINS, COLLEEN M.
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
25.5%; Score 479.5; DB 7; 37.4%; Pred. No. 2.4e-35; iive 53; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.4%; Score 477.5; DB 7; 37.7%; Pred. No. 3.5e-35; ive 54; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR PILING DATE: 2004-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PACENTIN VERSION 3.3
SEQ ID NO 262
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 262, Application US/11024959
Publication No. US20060010516A1
GENERAL INFORMATION:
APPLICANT: FORSTER, RICHARD L.
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Job time : 11.8631 secs

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42 YTOLOYIGEGAYGMVSSAYDHVRKTRVAIKKI-SPFEHOTYCORTLREIQILLRFRHENV 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 LWYRPPELLLGATKYGPAVDMWSVGCIFAELLHGKPIFPGKDEPEQLNKIFELCGAPDE- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 DINCIINMKARNYLQSLPSKTKVAW------AKLFPKSDSKALDLLDRMLTF 313
63 IVRLYDVVHTE----KKLTLVFEFLDQDLKKYLDACGDNGLEPYTVKSFLYQLLQGIAF 117
                                                                                                  101 IGIRDILRASTLEAMRD------VYIVQDLMETDLYKLL--KSQQLSNDHICYFL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 YOILRGLKYIHSANVIHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 ----INW------PGVSKIPWYNNFKPTRPMKRRLREVFRHFDRHALBLLERMLTL 307
                                     157 IHSANVLHRDLKPSNLLINTTCDLKICDFGLAR-IADPEHDHTGFLTEYVATRWYRAPEI 215
                                                     216 MINSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQIAHILGILGSPSQEDLACINM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:||: : :|||: | | || 308 DPSQRISAKDALDAEYFWADPLPCDPKSLPKYESSHEFQTKKKQQQRQHEBTAKRQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KERLKELIFOETARFQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                     276 KARNYLQSLPSKTKVAWAKLFPKS-DSKALDLLDRMLTFNPNKRITVAE 323
                                                                                                                                                  25.1%; Score 472.5; DB 7; Length 520; 34.2%; Pred. No. 2e-34; tive 56; Mismatches 116; Indels 63
                                                                                                                                                                                                          314 NPNKRITVAEEPFTFAMELDDLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 34.2
Matches 122, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 520
; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-272
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